

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 02:44:53 ; Search time 29.9342 Seconds  
(without alignments)  
324.190 Million cell updates/sec

Title: US-09-757-415A-1\_COPY\_11\_140

Perfect score: 696

Sequence: 1 DTVPNHRNKFVINDDG.....NNHQTELEVPRTPTPTTPG 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUTS-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	685	98.4	508	3	US-08-980-523-9
2	679	97.6	129	3	US-08-980-523-11
3	143.5	20.6	481	3	US-08-787-091-2
4	135	19.4	412	4	US-09-949-016-7584
5	134.5	19.3	145	4	US-09-270-767-57695
6	134.5	19.3	328	4	US-09-270-767-42405
7	79.5	11.4	412	4	US-09-949-016-11420
8	79	11.4	412	4	US-09-248-796A-20552
9	78	11.2	105	4	US-09-377-285B-5
10	78	11.2	1234	2	US-08-317-310A-15
11	78	11.2	1234	5	PCT-US95-13041-15
12	78	11.2	1242	4	US-09-508-691-1
13	78	11.2	1242	4	US-09-903-248-5
14	78	11.2	1242	4	US-09-903-199-5
15	78	11.2	1242	4	US-09-903-216-5
16	78	11.2	1242	4	US-09-903-063-5
17	78	11.2	1242	4	US-09-859-604-5
18	78	11.2	1243	2	US-08-557-139-2
19	77.5	11.1	112	3	US-08-980-523-10
20	77	11.1	38	3	US-08-787-091-9
21	76	10.9	505	4	US-09-270-767-41788
22	75	10.8	435	2	US-08-531-439B-4
23	74.5	10.7	709	4	US-09-489-847-132
24	72.5	10.4	153	4	US-09-270-767-32681
25	72.5	10.4	153	4	US-09-270-767-47898
26	72.5	10.4	541	3	US-09-134-001C-4481
27	68.5	9.8	342	4	US-09-543-681A-5131

28 68.5 9.8 1561 3 US-08-894-017-23 Sequence 23, Appl  
29 68.5 9.8 1561 4 US-09-456-474-23 Sequence 23, Appl  
30 68 9.8 159 4 US-09-508-691-5 Sequence 5, Appl  
31 68 9.8 1321 2 US-08-317-310A-64 Sequence 64, Appl  
32 67.5 9.7 118 3 US-08-936-165A-464 Sequence 464, Appl  
33 67.5 9.7 342 4 US-09-489-039A-14092 Sequence 14092, A  
34 67 9.6 144 4 US-09-134-000C-4435 Sequence 4435, Ap  
35 67 9.6 233 4 US-09-710-279-784 Sequence 784, App  
36 67 9.6 413 3 US-09-215-694-6 Sequence 6, Appl  
37 67 9.6 492 3 US-09-134-001C-3895 Sequence 3895, Ap  
38 66.5 9.6 1817 3 US-09-004-838-125 Sequence 125, App  
39 66 9.5 378 3 US-09-134-001C-5487 Sequence 5487, Ap  
40 66 9.5 441 4 US-09-270-767-47360 Sequence 47360, A  
41 65.5 9.4 237 4 US-09-710-279-182 Sequence 162, App  
42 65.5 9.4 380 4 US-09-710-279-1402 Sequence 1402, Ap  
43 65.5 9.4 794 4 US-09-134-001C-1050 Sequence 1050, Ap  
44 65.5 9.4 962 3 US-09-134-001C-4497 Sequence 4497, Ap  
45 65 9.3 268 4 US-09-438-185A-1041 Sequence 1041, Ap

#### ALIGNMENTS

RESULT 1  
US-08-980-523-9  
; Sequence 9, Application US/08980523  
; Patent No. 6310181  
; GENERAL INFORMATION:  
; APPLICANT: Kouhara, Haruhiko  
; APPLICANT: Spivak-Kroizman, Taly  
; APPLICANT: Lax, Irit  
; APPLICANT: Schllessinger, Joseph  
; TITLE OF INVENTION: ADAPTOR PROTEIN FRS2 AND  
; TITLE OF INVENTION: RELATED PRODUCTS AND METHODS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/980.523  
FILING DATE: December 1, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/21851  
FILING DATE: December 1, 1997  
APPLICATION NUMBER: 60/032.093  
FILING DATE: December 3, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 230/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 508 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-08-980-523-9

Query Match 98.4%; Score 685; DB 3; Length 508;  
Best Local Similarity 97.7%; Pred. No. 6.3e-77;  
Matches 127; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTPDNHNRKFKVINVDGDELGSGIMELTDTLILYTRKRDSVKWHYLCILRRYGYDSN 60  
Db 1 DTPDNHNRKFKVINVDGDELGSGIMELTDTLILYTRKRDSVKWHYLCILRRYGYDSN 60

Qy 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELVVP 120  
Db 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELVVP 120

Qy 121 RTPRTPTTPG 130  
Db 131 RTPRTPTTPG 140

## RESULT 2

US-08-980-523-11  
; Sequence 11, Application US/08980523  
; Patent No. 6310181  
; GENERAL INFORMATION:  
; APPLICANT: Kouhara, Haruhiko  
; APPLICANT: Spivak-Kroizman, Taly  
; APPLICANT: Lax, Irit  
; APPLICANT: Schlössinger, Joseph  
; TITLE OF INVENTION: ADAPTOR PROTEIN PRS2 AND  
; TITLE OF INVENTION: RELATED PRODUCTS AND METHODS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Fast-SEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
FILING DATE: December 1, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/21851  
FILING DATE: December 1, 1997  
APPLICATION NUMBER: 60/032,093  
FILING DATE: December 3, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 230/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-980-523-11

Query Match 97.6%; Score 679; DB 3; Length 129;  
Best Local Similarity 97.7%; Pred. No. 5.2e-77;

Matches 126; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTPDNHNRKFKVINVDGDELGSGIMELTDTLILYTRKRDSVKWHYLCILRRYGYDSN 60  
Db 1 DTPDNHNRKFKVINVDGDELGSGIMELTDTLILYTRKRDSVKWHYLCILRRYGYDSN 60

Qy 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELVVP 120  
Db 61 LFSFSGRRRCOTGGQIFAFKCARAEELFNMQLQEIOMNNSINVVEPVPVVERNNHOTELVVP 120

Qy 121 RTPRTPTTP 129  
Db 121 RTPRTPTTP 129

## RESULT 3

US-08-787-091-2  
; Sequence 2, Application US/08787091  
; Patent No. 6100386  
; GENERAL INFORMATION:  
; APPLICANT: Carpino, Nicholas A.  
; APPLICANT: Kobayashi, Ryuji  
; APPLICANT: Wisniewski, David G.  
; APPLICANT: Strife, Annabel O.C.  
; APPLICANT: Clarkson, Bayard D.  
; TITLE OF INVENTION: A No. 6100386el Human Gene/Protein Involved in  
; TITLE OF INVENTION: Chronic Myelogenous Leukemia  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/787,091  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/030,418  
FILING DATE: 01-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-05pa  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 481 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-787-091-2

Query Match 20.6%; Score 143.5; DB 3; Length 481;  
Best Local Similarity 29.5%; Pred. No. 3.7e-09;  
Matches 33; Conservative 20; Mismatches 50; Indels 9; Gaps 2;

Qy 24 GSGIMELTDTLILYTRKRDS-----VKWHYLCILRRYGYDSNLFSSFGRRRCOTGGQIF 77  
Db 172 GSYVLRVEAERLTLLTVGAQSQILEPLLSWPYTLRLRYGRDKWVMSFEAGRRCPSPGTF 231

Qy 78 AFKCARAEELFNMQLQEIOMNNSINVVE---EPVVERNNHOTELVVPTRTP 126  
Db 232 TFOTAQGNDFQAVETAHROKAGQAGQGHDLVRADSHSHEGVAEGKLPSPP 283

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RESULT 5
US-09-270-767-57695
; Sequence 57695, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57695
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57695

Query Match          19.3%; Score 134.5; DB 4; Length 145;
Best Local Similarity 24.8%; Pred. No. 9,1e-09;
Matches 31; Conservative 25; Mismatches 40; Indels 29; Gaps 3;

Qy      27 IMELTDELILYTKRDS--VKWHYLCURRYGYDSNLFSPFSGRRCQTGGIIFAPKCARA 84
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      5 MLOWTPTELQKSDLGATIAMWYRFIRKYGYRDGKFTFEAGRCKTTGEGVFTLDHTNP 64
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Qy      85 EELF-----NMLQETIMONNSINVVE-----BPVVERNNHQTEL 117
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db      65 QEVPRCHSAVMKSMKKLISGDSLSLTLECGENQFSAAGACGEPGSRSPLPSPSSNPHGGEF 124
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Qy      118 EVPRT 122
      |:|
Db      125 EINST 129

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RESULT 7
US-09-949-016-11420
; Sequence 11420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11420
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11420

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Query Match      11.4%; Score 79.5; DB 4; Length 412;
Best Local Similarity 20.8%; Pred. No. 0.3;
Matches 27; Conservative 32; Mismatches 48; Indels 23; Gaps 6;

Qy 2 TVPDNRHKPKVINVDGNGELGSGIMELT---DTLLILYTRGRDSVKWHY--LCLRRYG 56
      : : : : : : : : : : : : : : : : : : : : : :
Db 225 SIFQKRMRLNLTIVEND-----TPLELSKYVDISIIALTRNRRTRWYTCPLCGQFN 279

Qy 57 YDSNLSFSGRCQTCGQIFAFKCARAEELFMNLQEIIMQNINNVVEEPPV-----V 108
      : : : : : : : : : : : : : : : : : : : : : :
Db 280 ESSYLISHQ---RTHGEEK--PYDCNHCGRSFNNKTNLKNKRIHTGEKPYSCQCGKNF 334

```



```

; APPLICANT: SUN, Xiao Jian
; APPLICANT: PIERCE, Jacalyn H.
; TITLE OF INVENTION: THE IRS FAMILY OF GENES
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13041
; FILING DATE: Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/317,310
; FILING DATE: 03-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-022PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-13041-15

Query Match 11.2%; Score 78; DB 5; Length 1234;
Best Local Similarity 30.0%; Pred. No. 2.2;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDNLFSFESGRRCQTGGIFAFKCAAEELFNMQLQIMQNSINNVVEEPPVVERN 111
DB 206 IRRCGHSENFIEVGRSAVTGPGBFWMQ-----VDDSVVAQN 243

QY 112 NHOTELEVR 121
DB 244 MHETILEAMR 253

RESULT 12
US-09-508-691-1
; Sequence 1, Application US/09508691
; Patent No. 6498139
; GENERAL INFORMATION:
; APPLICANT: YAZAKI, YOSHIO
; APPLICANT: ASANO, TOMOICHIRO
; APPLICANT: KUBO, HIDEO
; APPLICANT: KANDA, AKIRA
; TITLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
; FILE REFERENCE: 4895-0019-OPCT
; CURRENT APPLICATION NUMBER: US/09/508,691
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PCT/JP98/04293
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: JP9-263719
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1242
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-508-691-1
Query Match 11.2%; Score 78; DB 4; Length 1242;
Best Local Similarity 30.0%; Pred. No. 2.2;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDNLFSFESGRRCQTGGIFAFKCAAEELFNMQLQIMQNSINNVVEEPPVVERN 111
DB 211 IRRCGHSENFIEVGRSAVTGPGBFWMQ-----VDDSVVAQN 248

QY 112 NHOTELEVR 121
DB 249 MHETILEAMR 258

RESULT 13
US-09-903-248-5
; Sequence 5, Application US/09903248
; Patent No. 6783758
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV5
; CURRENT APPLICATION NUMBER: US/09/903,248
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-248-5

Query Match 11.2%; Score 78; DB 4; Length 1242;
Best Local Similarity 30.0%; Pred. No. 2.2;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDNLFSFESGRRCQTGGIFAFKCAAEELFNMQLQIMQNSINNVVEEPPVVERN 111
DB 211 IRRCGHSENFIEVGRSAVTGPGBFWMQ-----VDDSVVAQN 248

QY 112 NHOTELEVR 121
DB 249 MHETILEAMR 258

RESULT 14
US-09-903-199-5
; Sequence 5, Application US/09903199
; Patent No. 6797696
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV4
; CURRENT APPLICATION NUMBER: US/09/903,199
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
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Result No.	Query			ID		Description
	Score	Match	Length	DB		
1	696	100.0	508	10	US-09-757-415A-1	Sequence 1, Appli
2	696	100.0	508	14	US-10-466-473-67	Sequence 67, Appl
3	696	100.0	521	15	US-10-276-774-2192	Sequence 2192, Ap
4	685	98.4	508	9	US-09-731-660A-1	Sequence 1, Appli
5	679	97.6	129	9	US-09-731-660A-3	Sequence 3, Appli
6	143.5	20.6	541	13	US-10-001-870-179	Sequence 179, App
7	141	20.3	359	9	US-09-789-919-58	Sequence 58, Appl
8	137.5	19.8	331	15	US-10-307-928A-6	Sequence 6, Appli
9	120.5	17.3	440	15	US-10-112-944-285	Sequence 285, App
10	111.5	16.0	289	14	US-10-106-698-6260	Sequence 6260, Ap
11	95.5	13.7	268	14	US-10-029-386-3396	Sequence 3396, A
12	95.5	13.7	268	15	US-10-264-049-2340	Sequence 2340, Ap
13	78	11.2	105	14	US-10-192-381-5	Sequence 5, Appli

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US-09-757-415A-1
; Sequence 1, Application US/09757415A
; Publication No. US20030040612A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; TITLE OF INVENTION: Methods of Identifying and Treating
; FILE REFERENCE: 2459-1-002N
; CURRENT APPLICATION NUMBER: US/09/757415A-1
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-415A-1

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104-10300

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Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

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RESULT 2
US-10-146-473-67
; Sequence 67, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-67

Query Match      100.0%; Score 696; DB 14; Length 508;
Best Local Similarity 100.0%; Pred. No. 8.1e-71;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 11 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 70

QY 61 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

RESULT 3
US-10-276-774-2192
; Sequence 2192, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2192
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2192

Query Match      100.0%; Score 696; DB 15; Length 521;
Best Local Similarity 100.0%; Pred. No. 8.4e-71;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 24 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 83

QY 61 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

Query Match      98.4%; Score 685; DB 9; Length 508;
Best Local Similarity 97.7%; Pred. No. 1.1e-69;
Matches 127; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 11 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 70

QY 61 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

RESULT 4
US-09-731-660A-1
; Sequence 1, Application US/09731660A
; Publication No. US20020086972A1
; GENERAL INFORMATION:
; APPLICANT: KOUHARA, HARUHIKO
; APPLICANT: SPIVAK-KROIZMAN, TALY
; APPLICANT: LAX, IRIT
; APPLICANT: SCHLESSINGER, JOSEPH
; TITLE OF INVENTION: ADAPTOR PROTEIN FRS2 AND RELATED PRODUCTS AND METHODS
; FILE REFERENCE: 038602/1023
; CURRENT APPLICATION NUMBER: US/09/731,660A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 08/980,523
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/032,093
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-660A-1

Query Match      98.4%; Score 685; DB 9; Length 508;
Best Local Similarity 97.7%; Pred. No. 1.1e-69;
Matches 127; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 60
Db 11 DTVPDHNRKFKVINVDGNGELSGIMELTDTLLYTRKDSVKWHYLCRLRYGYDSN 70

QY 61 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 120
Db 71 LFSFESGRRCTGGQGFAPKCARAEELFNMLOEIMQNNNSINVVEPVPVVRNNHOTELEVP 130

QY 121 RTPRTPTTPG 130
Db 131 RTPRTPTTPG 140

RESULT 5
US-09-731-660A-3
; Sequence 3, Application US/09731660A
; Publication No. US20020086972A1
; GENERAL INFORMATION:
; APPLICANT: KOUHARA, HARUHIKO
; APPLICANT: SPIVAK-KROIZMAN, TALY
; APPLICANT: LAX, IRIT
; APPLICANT: SCHLESSINGER, JOSEPH
; TITLE OF INVENTION: ADAPTOR PROTEIN FRS2 AND RELATED PRODUCTS AND METHODS
; FILE REFERENCE: 038602/1023
; CURRENT APPLICATION NUMBER: US/09/731,660A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 08/980,523
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/032,093
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 129
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-660A-3

Query Match
Best Local Similarity 97.6%; Score 679; DB 9; Length 129;
Matches 126; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTVPNHRNKFVINVDGNGELGSGIMELTDTLILYTRKDSVKWHYLCRLRYGYDSN 60
Db 1 DTVPNHRNKFVINVDGNGELGSGIMELTDTLILYTRKDSVKWHYLCRLRYGYDSN 60
QY 61 LFSFSGRCQCGGIFAFKARAELEFNMLQEIOMNNSINVVEBPVVERNHHQTELEVP 120
Db 61 LFSFSGRCQCGGIFAFKARAELEFNMLQEIOMNNSINVVEBPVVERNHHQTELEVP 120
QY 121 RTPRTPTTP 129
Db 121 RTPRTPTTP 129

RESULT 6
US-10-001-870-179
; Sequence 179, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yengming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 179
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-870-179

Query Match
Best Local Similarity 20.6%; Score 143.5; DB 13; Length 541;
Matches 33; Conservative 20; Mismatches 50; Indels 9; Gaps 2;

QY 24 GSGIMELTDTLILYTRKDS-----VKWHYLCRLRYGYDSNLFSPESGRCQCGGIF 77
Db 248 GSYLVRAERITLLTVGAQSQILEPLLSWPYTLRLRYGRDKVMFSEAGRCPCSPGTF 307
QY 78 AFKARAELEFNMLQEIOMNNSINVVE---BPVVERNHHQTELEVPRTPTP 126
Db 308 TQTQAGNDIFQAVETAIHRQAQKAGQGHDLVLRADSHGEVAGKUPSP 359

RESULT 7
US-09-789-919-58
; Sequence 58, Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor
; APPLICANT: Moore, Kateri
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789,919
; CURRENT FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 58
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; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-789-919-58

Query Match
Best Local Similarity 20.3%; Score 141; DB 9; Length 359;
Matches 36; Conservative 20; Mismatches 47; Indels 24; Gaps 3;

QY 23 LSGIMEITDTLILYTRKDSVKWHYLCRLRYGYDSNLFSPESGRCQCGGIFAFKCA 82
Db 184 LQDDIQLRET-----SKPQACFSWPYRFLRKYGSDKGVSEAGRCDCSGELFAFSSP 238
QY 83 RAELEFNMLQEIOMNNSINVVE-----BPVVERNHHQTELEVPRTPTP 124
Db 239 RAPDTCGVAAAIARQRERLPELAMPCCPLPRALSLPSLEPPGELREVAAPGFELETPRK 298
QY 125 TP-TTPG 130
Db 299 LPLTDPG 305

RESULT 8
US-10-307-928A-6
; Sequence 6, Application US/10307928A
; Publication No. US20030229016A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Catterton, Elina
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Saasha)
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; FILE REFERENCE: 24102-502D
; CURRENT APPLICATION NUMBER: US/10/307,928A
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/381,495
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/383,744
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/384,024
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/401,788
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: CuraSeqList version 0.1
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; SEQ ID NO 6
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-928A-6

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Query Match 19.8%; Score 137.5; DB 15; Length 331;  
Best Local Similarity 31.5%; Pred. No. 5e-07;  
Matches 34; Conservative 19; Mismatches 42; Indels 13; Gaps 3;

Qy 24 GSGIMELTDELIYTRKRDVSK--WHYLCRLRYGYDSNLFSPESGRRRCOTGGQIFAFK 80

Dd 153 GECTMQITHENIYLDIHNAAKVLMVWPLSSRLRYGRDSTWTFPSGRCMDTGEGLTFQ 212

Qy	81	CARAEELFNMLQEI	MONNSIN	VVEE-----	PVERN	NHQTELEV	PRT 122
					:	:	
			:	:	:	:	
Dp	213	TREGE----	MIYOKV	SATLAI	AEOHRL	MEOKAR	LOTSIPMT 256
			:	:	:	:	
			:	:	:	:	

```

RESULT 9
US-10-112-944-285
; Sequence 285, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: NO. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides

```

Query Match 17.3%; Score 120.5; DB 15; Length 440;  
Best Local Similarity 29.7%; Pred. NO. 6.6e-05;  
Matches 35; Conservative 16; Mismatches 38; Indels 29; Gaps 5;

Qy 23 LGSIMELTDTE--LILYTRKRDSVKWHYLCRLRRGYDSNLFSPSGRRRCOTGGIFAFK 80  
 184 LGPDAIQUREAKGTQALYS-----WPHYFLRLKLSGDKGVSPFSEAGRRCHSGEGLFAFS 236  
 Db

Qy	81	CARABELNMLQEI	QNNNSIN	VVEPVV	RNNH	OTEL-----	EV	RT	PT	PT	-----	TPG	130
		:		:	:		:	:	:	:	:	:	
Db	237	TPCAPDL-----	CRAVAGAI	QRQRER	DEL	TR	TP	QC	PL	PR	AT	SL	282
		:		:	:		:	:	:	:	:	:	

## RESULT 10

US-10-106-698-6260  
; Sequence 6260, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:

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Query Match      16.0%; Score 111.5; DB 14; Length 289;
Best Local Similarity 31.2%; Pred. No. 0.0004;
Matches 20; Conservative 15; Mismatches 26; Indels 3; Gaps 1;
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QY	28	MELTDTTELLYTRKRDVK---	WHYLCRLRRYGYDSNLFSPESGRRCQTGGQIFAPKCARA	84
DB	202	LOITHTENYLDIHNPRVKLVSWXLCXXRRYGRDATRFTFEAGRMCDAGEGLYFTQFQG	261	

Qy	85	EEF	88
			::
Dp	262	EQIY	265

RESULT 11  
US-10-029-386-33396  
; Sequence 33396, Application US/10029386  
; Publication No. US20030194704A1

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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P56945, EVALUJE 2.00e-03
US-10-029-386-33396

Query Match      13.7%; Score 95.5; DB 14; Length 268;
Best Local Similarity 27.5%; Pred. No. 0.025;
Matches 19; Conservative 16; Mismatches 31; Indels 3; Gaps 1;

QY 61 LPSFSGRCQTGGIFAFKCAAEELFNNLQEIIMQNNNSINVVE---EPVVERNHHQTEL 117
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2 MFSFEAGRCPSGPGTFTTQAGNDIFQAVETAIHROKAGQKAGQGHDLVLRADSHGEV 61
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 118 EVPTPTPT 126
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 AEGKLPSP 70
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
US-10-264-049-2340
; Sequence 2340, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2340
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2340

Query Match      13.7%; Score 95.5; DB 15; Length 268;
Best Local Similarity 27.5%; Pred. No. 0.025;
Matches 19; Conservative 16; Mismatches 31; Indels 3; Gaps 1;

QY 61 LPSFSGRCQTGGIFAFKCAAEELFNNLQEIIMQNNNSINVVE---EPVVERNHHQTEL 117
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2 MFSFEAGRCPSGPGTFTTQAGNDIFQAVETAIHROKAGQKAGQGHDLVLRADSHGEV 61
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 118 EVPTPTPT 126
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 AEGKLPSP 70
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13
US-10-192-381-5
; Sequence 5, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
; FILE REFERENCE: JHUI580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
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; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-192-381-5

Query Match      11.2%; Score 78; DB 14; Length 105;
Best Local Similarity 30.0%; Pred. No. 0.73;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDSNLSFSGRCQTGGIFAFKCAAEELFNNLQEIIMQNNNSINVVEPVVERN 111
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 51 IRRCGHSENFFFIEVGRSAVTGPGBFMMQ-----VDDSVVAQN 88
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 112 NHQTELEVP 121
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 89 MHETILEAMR 98
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-09-731-660A-2
; Sequence 2, Application US/09731660A
; Publication No. US20020086972A1
; GENERAL INFORMATION:
; APPLICANT: KOUHARA, HARUHIKO
; APPLICANT: SPIVAK-KROIZMAN, Taly
; APPLICANT: LAX, Irit
; APPLICANT: SCHLESSINGER, JOSEPH
; TITLE OF INVENTION: ADAPTOR PROTEIN PRS2 AND RELATED PRODUCTS AND METHODS
; FILE REFERENCE: 038602/1023
; CURRENT APPLICATION NUMBER: US/09/731,660A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 08/980,523
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/032,093
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: PTB domain of IRS-1
; OTHER INFORMATION: IRS-1
US-09-731-660A-2

Query Match      11.2%; Score 78; DB 9; Length 114;
Best Local Similarity 30.0%; Pred. No. 0.82;
Matches 21; Conservative 7; Mismatches 20; Indels 22; Gaps 1;

QY 52 LRRYGYDSNLSFSGRCQTGGIFAFKCAAEELFNNLQEIIMQNNNSINVVEPVVERN 111
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 59 IRRCGHSENFFFIEVGRSAVTGPGBFMMQ-----VDDSVVAQN 96
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 112 NHQTELEVP 121
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 97 MHETILEAMR 106
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 15
US-10-694-874-3
; Sequence 3, Application US/10694874
; Publication No. US2004009713A1
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2005, 03:11:53 ; Search time 224.079 Seconds  
(without alignments)  
949.290 Million cell updates/sec

Title: US-09-757-415a-1\_COPY\_11\_140  
Perfect score: 696  
Sequence: 1 DTVPDHRNFKVINVDDG.....NNHQTELEVPRTPTPTPG 130

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-USER=US09757415 @CGN 1.1.93 @runat\_07022005\_160041\_26836 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143.5	20.6	1446	3	US-08-787-091-1
2	137.5	19.8	1146	4	US-09-620-312D-854
3	135.5	19.3	1239	4	US-09-949-016-1713
4	134.5	19.3	531	4	US-09-270-767-26283
5	134.5	19.3	1363	4	US-09-270-767-10813
6	133.5	19.2	914	4	US-09-620-312D-855
7	124.5	17.9	2735	4	US-09-620-312D-842
c 8	100	14.4	601	4	US-09-949-016-59090
c 9	100	14.4	8291	4	US-09-949-016-13455
c 10	83	11.9	1813	3	US-09-453-7028-91
c 11	82.5	11.9	415	4	US-09-621-976-12526
12	79.5	11.4	2959	4	US-09-949-016-5549

13	79.5	11.4	16782	4	US-09-949-016-17291	Sequence 17291, A
14	79	11.4	1239	4	US-09-248-796A-6449	Sequence 6449, Ap
15	78	11.2	5828	4	US-09-023-655-1386	Sequence 1386, Ap
16	78	11.2	5828	4	US-09-903-248-6	Sequence 6, Appli
17	78	11.2	5828	4	US-09-903-199-6	Sequence 6, Appli
18	78	11.2	5828	4	US-09-903-216-6	Sequence 6, Appli
19	78	11.2	5828	4	US-09-903-063-6	Sequence 6, Appli
20	78	11.2	5828	4	US-09-859-604-6	Sequence 6, Appli
21	78	11.2	6152	1	US-08-557-139-1	Sequence 1, Appli
22	77.5	11.1	698	3	US-08-896-164-44	Sequence 44, Appli
23	75	10.8	1600	2	US-08-531-439B-3	Sequence 3, Appli
24	75	10.8	1600	4	US-09-023-655-1505	Sequence 1505, Ap
25	74.5	10.7	1000	4	US-09-270-767-2197	Sequence 2197, A
26	74.5	10.7	1461	4	US-09-270-767-11592	Sequence 11592, A
27	74.5	10.7	2209	4	US-09-489-847-16	Sequence 16, Appli
28	74	10.6	1664976	4	US-08-916-421B-1	Sequence 1, Appli
29	74	10.6	1664976	4	US-09-692-570-1	Sequence 1, Appli
c 30	74	10.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 31	74	10.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 32	73.5	10.6	1299	4	US-09-891-641-49	Sequence 49, Appli
33	73.5	10.6	1746	4	US-09-248-796A-1302	Sequence 1302, Ap
34	72.5	10.4	461	4	US-09-270-767-1052	Sequence 1052, Ap
35	72.5	10.4	461	4	US-09-270-767-16334	Sequence 16334, A
c 36	72.5	10.4	654	4	US-09-270-767-11316	Sequence 11316, A
37	72.5	10.4	1626	3	US-09-134-001C-1644	Sequence 1644, Ap
c 38	72.5	10.4	3086	4	US-09-710-279-3956	Sequence 3956, Ap
39	72	10.3	453	4	US-09-270-767-3433	Sequence 3433, Ap
40	72	10.3	453	4	US-09-270-767-18715	Sequence 18715, A
41	72	10.3	1896	4	US-09-949-016-5724	Sequence 5724, Ap
42	72	10.3	2313	3	US-09-370-838-157	Sequence 157, App
43	72	10.3	2313	4	US-09-854-133-157	Sequence 157, App
44	72	10.3	15062	3	US-09-004-838-89	Sequence 89, Appli
45	71	10.2	12286	4	US-09-902-540-1035	Sequence 1035, Ap

ALIGNMENTS

RESULT 1

US-08-787-091-1  
; Sequence 1, Application US/08787091  
; Patent No. 6100386  
; GENERAL INFORMATION:  
; APPLICANT: Carpino, Nicholas A.  
; APPLICANT: Kobayashi, Ryuji  
; APPLICANT: Wisniewski, David G.  
; APPLICANT: Strife, Annabel O'C.  
; APPLICANT: Clarkson, Bayard D.  
; TITLE OF INVENTION: A No. 6100386el Human Gene/Protein Involved in  
; TITLE OF INVENTION: Chronic Myelogenous Leukemia  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/787,091  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/030,418  
; FILING DATE: 01-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL96-05pa

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1443
US-08-787-091-1
Alignment Scores:
Pred. No.: 2,728-10 Length: 1446
Score: 143.50 Matches: 33
Percent Similarity: 47.32% Conservatives: 20
Best Local Similarity: 29.45% Mismatches: 50
Query Match: 20.62% Indels: 9
DB: 3 Gaps: 2
US-09-757-415A-1_COPY_11_140 (1-130) x US-08-787-091-1 (1-1446)
QY 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuLeuLeuTyrThrArgLysArgAsp 43
DB 514 GGCTCTACGCTGCTGAGGTGAGGCTGAAAGCGTGAAGCTCTCTGACCTGGGGGCCGCG 573
QY 44 Ser-----ValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyr 57
DB 574 AGTCAGATACTGGAGCCACTGCTGCTGCTGGCCCTACACTCTGTGGTGGCTATGGCCGG 633
QY 58 AspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyLeuPhe 77
DB 634 GACAAAGTCATGTTCTCTTTTCGAGGCGCGCGCGCTGCCCCCTCAGGGCCCTGGAACTTC 693
QY 78 AlaPheLysCysAlaAlaGluGluLeuPheAsnMetLeuGlnGluLeuMetGlnAsn 97
DB 694 ACCTTCCAGAGCGGCACAGGGAATGACATCTTCCAGGCGATGTGAGACTGCCATCCACCGG 753
QY 98 AsnSerIleAsnValValGlu-----GluProValValGluArgAsnAsnHisGln 114
DB 754 CAGAAAGGCCAGGAAAGGCCGACAGGGCGCAGCATGTTCTCAGAGCTGACTGCCATGAA 813
QY 115 ThrGluLeuGluValProArgThrProArgThrPro 126
DB 814 GGGGAGGTGGCAGAGGGGAAGTTGCCCTTCCCCACCT 849
RESULT 2
; Sequence 854, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 854
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(1122)
US-09-620-312D-854
Alignment Scores:
Pred. No.: 1,398-09 Length: 1146
Score: 137.50 Matches: 34
Percent Similarity: 49.07% Conservatives: 19
Best Local Similarity: 31.48% Mismatches: 42
Query Match: 19.76% Indels: 13
DB: 4 Gaps: 3
US-09-757-415A-1_COPY_11_140 (1-130) x US-09-620-312D-854 (1-1146)
QY 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuLeuLeuTyrThrArgLysArgAsp 43
DB 565 GGTGAATGCACAATGCAGTCACTCATGAAAATATCTATCTCTGGATATCCACAATGCC 624
QY 44 SerValLys-----TrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
DB 625 AAGGTCAAACTGGTGTGATGTGGCTCTCAGCTCAGTGGAGAGATCGGTGCGGACTCAACG 684
QY 61 LeuPheSerPheGluSerGlyValArgArgCysGlnThrGlyGlnGlyLeuPheAlaPheLys 80
DB 685 TGGTTACGTTTGACTCAGGAAGATGTGTGACACAGGAGAGGACTATTCTACTTTCAA 744
QY 81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluLeuMetGlnAsnAsnSerIle 100
DB 745 ACAAGGGAAGGAGAA-----ATGATCTATCAGAAGGTTTCATTCTCGCACACTG 792
QY 101 AsnValValGluGlu-----ProValValGluArgAsnAsnHisGln 114
DB 793 GCCATAGCTGAGCAACATGAAGATTAATGCTAGAAATGGAACAGAGGCCCGGCTTCAG 852
QY 115 ThrGluLeuGluValProArgThr 122
DB 853 ACAAGCTTGACTGAACCAATGACA 876
RESULT 3
US-09-949-016-1713
; Sequence 1713, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1713
; LENGTH: 1239
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; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1713

Alignment Scores:
Pred. No.: 3, 02e-09 Length: 1239
Score: 135.50 Matches: 37
Percent Similarity: 49.07% Conservative: 16
Best Local Similarity: 34.26% Mismatches: 35
Query Match: 19.47% Indels: 20
DB: 4 Gaps: 4

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-949-016-1713 (1-1239)
Qy 38 TyrThrArgLysArgAsp---SerValLys-TrpHisTyrLeuCysLeuArgArgTyrGl 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 549 TGGGCCCGAGCGAGGAGCCAGCTACAGCTGGCCCTACAGGTTTCTGCGGCGCTTGG 608
Qy 56 yTyrAspSerAsnLeuPheSerPheGluSerClyArgArgCysGlnThrGlyGlnGlyTl 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 609 GCGGACAAAGTAACCTTTTCTTTGAGCGAGCGCTCGCTCGCTCTCTGGAGAGGGCAA 668
Qy 76 ePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMet-- 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 669 CTTTGAGTTCGAACCCCGGAGGCAATGAGATCTTCTTGGCCCTGGAGAGGCCATCTC 728
Qy 96 ----GlnAsnAsnSerIleAsnValValGluGluProValValGluArgAsnAsnHisGl 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 729 TGCCCAAGAAGATGCTGACCCGCTACACCCCAACCG-----CAGCCAGCCAC 776
Qy 114 nThrGluLeuGluValProArg-----Th 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 777 AATCCCGCGCTCGGTGCGCCGCGCTGATAGCCCTACTCTCGGCGCATGACTCACTGCC 836
Qy 122 rProArgThrProThrThrPro 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 837 GCCGCTTCACCCACCAACACCG 858

RESULT 4
US-09-270-767-26283
; Sequence 26283, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26283
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26283

Alignment Scores:
Pred. No.: 1, 17e-09 Length: 531
Score: 134.50 Matches: 31
Percent Similarity: 44.80% Conservative: 25
Best Local Similarity: 24.80% Mismatches: 40
Query Match: 19.32% Indels: 29
DB: 4 Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-270-767-26283 (1-531)
Qy 27 IleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAspSer----- 44
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 ATGCTCCAAATGACGCCCATCTGAACCTTCAGTTGAAATCGGAGGATTTGGCGGCCACAATC 72
Qy 45 ValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPheSerPhe 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 GCCATGTGGCCATATCGTTTCATTAGGAAGTACGGCTATCGCATGGCAAGTTCACCTTT 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Qy	65	GluserylArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAla	84
Db	133	GAGCGGGCAGAAAATCACCACCGGCGAAGGCGGTTTTTCA	192
Qy	85	GlulGlulPhe	97
Db	193	CAGGAGGTATTCGCTGCATGTCGCGCAAGATGAAGTCGATGAAGAAACTGATTAGCGGC	252
Qy	98	AsnSerIleAsnValValGlu	104
Db	253	GATAGTCTGAGCACCTTGGAGTGGGTGAGAAATCAGTTTAGTGGCGCAGCTGGCATGGAG	312
Qy	105	-----GluProValValGluArgAsnAsnHisGlnThrGluLeu	117
Db	313	CCCGTTTCGGAGAGCCCACTGCCACCATCACCGTCGAGTAATCCCCACGGTGGCGAGTTC	372
Qy	118	GluValProArgThr	122
Db	373	GAGATCAACTCAACG	387
RESULT 5			
US-09-270-767-10813			
; Sequence 10813, Application US/09270767			
; Patent No. 6703491			
; GENERAL INFORMATION:			
; APPLICANT: Homburger et al.			
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster			
; FILE REFERENCE: File Reference: 7326-094			
; CURRENT APPLICATION NUMBER: US/09/270,767			
; CURRENT FILING DATE: 1999-03-17			
; NUMBER OF SEQ ID NOS: 62517			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 10813			
; LENGTH: 1363			
; TYPE: DNA			
; ORGANISM: Drosophila melanogaster			
US-09-270-767-10813			
Alignment Scores:			
Pred. No.: 4,86e-09 Length: 1363			
Score: 134.50 Matches: 31			
Percent Similarity: 44.80% Conservative: 25			
Best Local Similarity: 24.80% Mismatches: 40			
Query Match: 19.32% Indels: 29			
DB: 4 Gaps: 3			
US-09-757-415A-1_COPY_11_140 (1-130) x US-09-270-767-10813 (1-1363)			
Qy	27	IleMetGluLeuThrAspThrGluLeuIleLeuTyThrArgLysArgAspSer	44
Db	845	ATGCTCCAAATGAGCCCACTGAACCTTCAGTTGAAATCGGAGGATTTGGCGCCACAATC	904
Qy	45	ValLysTrpHisTyLeuCysLeuArgArgTyGlyTyRAspSerAsnLeuPheSerPhe	64
Db	905	GCCATGTGGCCATATCGTTTCATTAGGAAGTAGCGCTATCCGATGCGCAAGTTTCACCTTT	964
Qy	65	GluserylArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAla	84
Db	965	GAGCGGGCAGAAAATCACCACCGGCGAAGGCGTTTTTCA	1024
Qy	85	GlulGlulPhe	97
Db	1025	CAGGAGGTATTCGCTGCATGTCGCGCAAGATGAAGTCGATGAAGAAACTGATTAGCGGC	1084
Qy	98	AsnSerIleAsnValValGlu	104
Db	1085	GATAGTCTGAGCACCTTGGAGTGGGTGAGAAATCAGTTTAGTGGCGCAGCTGGCATGGAG	1144
Qy	105	-----GluProValValGluArgAsnAsnHisGlnThrGluLeu	117
Db	1145	CCCGTTTCGGAGAGCCCACTGCCACCATCACCGTCGAGTAATCCCCACGGTGGCGAGTTC	1204

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RESULT 4
US-09-270-767-26283
; Sequence 26283, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26283
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26283

Alignment Scores:
Pred. No.:      1.17e-09      Length:      531
Score:          134.50      Matches:      31
Percent Similarity: 44.80%      Conservative: 25
Best Local Similarity: 24.80%      Mismatches:   40
Query Match:      19.32%      Indels:       29
DB:               4          Gaps:         3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-270-767-26283 (1-531)

Qy 27 IleMetGluLeuThrAspThrGluLeuIleLeuTyThrArgLysArgAspSer----- 44
      ::::::::::::::::::::|:::
Db 13 ATGCTCCAAATGACGCCCCACTGAACTTCAGITGAAATCGAGGATTTCGGCGCCACAATC 72
      ::::::::::::::::::::|:::
Qy 45 ValLysTrpHisTyLeuCysLeuAArgTyGlyTyThrAspSerAsnLeuPheSerPhe 64
      ::::::::::::::::::::|:::
Db 73 GCCATGTGGCCATATCGTTTCTAGGAAGTACGGCTATCGCGATGCGCAAGTTCACCTTT 132
      ::::::::::::::::::::|:::

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US-09-757-415A-1_COPY_11_140 (1-130) x US-09-270-767-10813 (1-1363)					
Alignment Scores:					
Pred. No.:	4.86e-09	Length:	1363		
Score:	134.50	Matches:	31		
Percent Similarity:	44.80%	Conservative:	25		
Best Local Similarity:	24.80%	Mismatches:	40		
Query Match:	19.32%	Indels:	29		
DB:	4	Gaps:	3		
US-09-757-415A-1_COPY_11_140 (1-130) x US-09-270-767-10813 (1-1363)					
Qy	27	IleMetGluLeuThrAspThrGluLeuIleuTyThrArgLysArgAppSer-----	44		
Db	845	ATGCTCCAAATGAGGCCCACTGAACCTTCAGTTGAAATCGGAGGAGTATTGGCGGCCACAATC	904		
Qy	45	VallYstfPHisTVrLeuCysLeuAtgArGTyTGlyTYrAspSerAsnLeuPheSerPhe	64		
Db	905	GCCATGTGGCCCATATCGTTTCATTAGGAAGTAGCGCTATCGCATGCAGAGTTCACACTTT	964		
Qy	65	GluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAla	84		
Db	965	GAGCGGGCAGAAAATGCACCACCGGCGAAGGGCTTTTTTCACCTCTGGATCACACCAATCCA	1024		
Qy	85	GluGluLeuPhe-----AsnMetLeuGlnGluIleMetGlnAsn	97		
Db	1025	CAGAGGTATTCGCTGCATGTCGGCCAGATGAAGTCGATGAAGAATACTGATTAGCGGC	1084		
Qy	98	AsnSerIleAsnValValGlu-----	104		
Db	1085	GATAGTCTGAGCACCTTGGAGTGGGTGAGAACATCAGTTTAGTCGGCAGCTGGCATGGAG	1144		
Qy	105	-----GluProValValGluArgAsnAsnHisGlnThrGluLeu	117		
Db	1145	CCCGGTTCCGAAGCCCACTGCCACCATCACCGTCGAGTAATCCCACGTCGGCGATTC	1204		

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Qy 118 GluValProArgThr 122
|||:::
Db 1205 GAGATCACTCAACG 1219

RESULT 6
US-09-620-312D-855
; Sequence 855, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: John Tillinghast
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 855
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(867)
US-09-620-312D-855

Alignment Scores:
Pred. No.: 3.7e-09 Length: 914
Score: 133.50 Matches: 33
Percent Similarity: 48.62% Conservative: 20
Best Local Similarity: 30.28% Mismatches: 43
Query Match: 19.18% Indels: 13
DB: 4 Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-620-312D-855 (1-914)
Qy 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyThrArgLysArgAsp 43
|||:::
Db 565 GGTGAATGCACATGCAGTCACTCATGAAATATCTATCTCTGGGATATCCACATGCC 624

Qy 44 SerValLys-----TriHisTyLeuCysLeuArgArgTyGlyTyArgSerAsn 60
|||||
Db 625 AAGGTCMAACTGGTGATGGCTCTCAGCTCACTGAGGAGATACGGTCGGGACTCAACG 684

Qy 61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
|||||
Db 685 TGGTTCACTTTGAGTCAGGAAGATGTGTGACACAGGAGAGGACTATTACTTTTCAA 744

Qy 81 CysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerile 100
|||||
Db 745 ACAAGGGAGAGAGAA-----ATGATCTATCAGAAAGGTTCAATTCTCGCACACTG 792

Qy 101 AsnValGluGluProValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
|||||
```

```
Db 793 GCCATAGCTGAGCAA-----CATGAAGATTAAATCTAGAAATGGAA 834
|||:::
Qy 121 ArgThrProArgThrProThrProThrPro 129
|||
Db 835 CAGAAAGCCCGGTAAGCCCTTCCT 861

RESULT 7
US-09-620-312D-842
; Sequence 842, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 842
; LENGTH: 2735
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (334)..(1314)
US-09-620-312D-842

Alignment Scores:
Pred. No.: 3.79e-07 Length: 2735
Score: 124.50 Matches: 31
Percent Similarity: 46.73% Conservative: 19
Best Local Similarity: 28.97% Mismatches: 48
Query Match: 17.89% Indels: 9
DB: 4 Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-620-312D-842 (1-2735)
Qy 28 MetGluLeuThrAspThrGluLeuIleLeuTyThrArgLysArgAspSerValLys--- 46
|||||
Db 802 CTGCAGATCACCCAGAGAACATCTACCTCTGGGATCCACACCCCGTGTGAAGCTC 861

Qy 47 -----TriHisTyLeuCysLeuArgArgTyGlyTyArgSerAsnLeuPheSerPhe 64
|||||
Db 862 GTCTCGCGCCCTCTGCTCACTGCGCGCTATGCGCGGATGCCACACGCTTTACCTTC 921

Qy 65 GluSerGlyArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAla 84
|||||
Db 922 GAGGCTGCCCGGATGTGTGATGCTGGGAGAGACTCTATACCTTCACACACAGAGGGG 981

Qy 85 GluGluLeuPheAsnMetLeuGlnGluIleMet-----GlnAsnAsnSer 99
|||||
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Db 982 GAGCAGATTTACCAGCGCGTCCACAGTGCACAGTGCACCCCTGCCATCGCAGAGCAGCACAGCGG 1041  
Qy 100 IleAsnValValGluGluProValValGluArgAsnAsnHisGlnThrGlu----LeuGlu 118  
Db 1042 GTCCTCTGGAATGGAGAGAACGTGAGGCTGCTGAACAAGGGCAGGCAACATTACTCG 1101  
Qy 119 ValProArgThrProArgThr 125  
Db 1102 TATCCCTGCACCCAGGACC 1122

RESULT 8  
US-09-949-016-59090/c  
; Sequence 59090, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59090  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-59090

Alignment Scores:  
Pred. No.: 0.000126 Length: 601  
Score: 100.00 Matches: 26  
Percent Similarity: 46.34% Conservative: 12  
Best Local Similarity: 31.71% Mismatches: 26  
Query Match: 14.37% Indels: 18  
DB: 4 Gaps: 3

US-09-757-415A-1\_COPY\_11\_140 (1-130) x US-09-949-016-59090 (1-601)

Qy 62 PheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyLeuPheAlaPheLysCys 81  
Db 462 TTTTCCTTTGAGCGAGCGCGTCTGCTGCTGAGAGGGCAACTTTGAGTTGGAAC 403  
Qy 82 AlaArgAlaGluGluLeuPheAsnMetLeuGlnGluileMet-----GlnAsnAsnSer 99  
Db 402 CGGCAAGGCAATGAGATCTTCTGGCCCTGGAAGAGGCCATCTCTGCCAGAGAATGCT 343  
Qy 100 IleAsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluVal 119  
Db 342 GCACCGGTACACCCACCG-----CAGCCAGCCCAATCCCGCGCTGCTG 295  
Qy 120 ProArg-----ThrProArgThrProThr 127  
Db 294 CCGCGCGCTGATAGCCCTTACTCTGCGCGCATGACTCTGCGCGCGCTTCACCCACC 235  
Qy 128 ThrPro 129  
Db 234 ACACCG 229

RESULT 9  
US-09-949-016-13455  
; Sequence 13455, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13455  
; LENGTH: 8291  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13455

Alignment Scores:  
Pred. No.: 0.00663 Length: 8291  
Score: 100.00 Matches: 26  
Percent Similarity: 46.34% Conservative: 12  
Best Local Similarity: 31.71% Mismatches: 26  
Query Match: 14.37% Indels: 18  
DB: 4 Gaps: 3

US-09-757-415A-1\_COPY\_11\_140 (1-130) x US-09-949-016-13455 (1-8291)

Qy 62 PheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyLeuPheAlaPheLysCys 81  
Db 5677 TTTTCCTTTGAGCGAGCGCGTCTGCTGCTGAGAGGGCAACTTTGAGTTGGAAC 5736  
Qy 82 AlaArgAlaGluGluLeuPheAsnMetLeuGlnGluileMet-----GlnAsnAsnSer 99  
Db 5737 CGGCAAGGCAATGAGATCTTCTGGCCCTGGAAGAGGCCATCTCTGCCAGAGAATGCT 5796  
Qy 100 IleAsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluVal 119  
Db 5797 GCACCGGTACACCCACCG-----CAGCCAGCCCAATCCCGCGCTGCTG 5844  
Qy 120 ProArg-----ThrProArgThrProThr 127  
Db 5845 CCGCGCGCTGATAGCCCTTACTCTGCGCGCATGACTCTGCGCGCGCTTCACCCACC 5904  
Qy 128 ThrPro 129  
Db 5905 ACACCG 5910

RESULT 10  
US-09-453-702B-91/c  
; Sequence 91, Application US/09453702B  
; Patent No. 6365723  
; GENERAL INFORMATION:  
; APPLICANT: Blattner, Frederick R.  
; Burland, Valerie  
; Perna, Nicole T.  
; Plunkett, Guy  
; Welch, Rod  
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 8.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/453,702B



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Db 963 ACTCGAATCGAGGACNAGGAGATGTACACTTGTCCACTGTGTGGGAAACAGTTTAAT 1022
QY 57 TyAspSerAsnLeuPheSerPheGluSerGlyArgCysGlnThrGlyGlnGlyIle 76
Db 1023 GAAAGTCTTACCTATTTCCACCAG-----AGGACCCACACTCGAGAGAAAA--- 1070
QY 77 PheAlaPheLysCysAlaAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGln 96
Db 1071 ---CCCTATGACTGTAACTACTGTGGGAAAGCTTCAATCATATAAAACAACCTCAATAA 1127
QY 97 AsnAsnSerIleAsnValValGluGluProVal-----Val 108
Db 1128 CATGACGGAATTCATACAGAGAGAAACCTTATTCCTGTTCTCAGTGTGGAAAAAACTTC 1187
QY 109 GluArgAsnAsnHisGlnThrGluLeuGlu 118
Db 1188 CGTCAGAAATCTCATCGGAGTCGTCATGAA 1217

RESULT 13
US-09-949-016-17291
; Sequence 17291, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17291
; LENGTH: 16782
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17291

Alignment Scores:
Pred. No.: 16.8 Length: 16782
Score: 79.50 Matches: 27
Percent Similarity: 45.38% Conservative: 32
Best Local Similarity: 20.77% Mismatches: 48
Query Match: 11.42% Indels: 23
DB: 4 Gaps: 6

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-949-016-17291 (1-16782)
QY 2 ThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGlyAsn 21
Db 12681 TCATTCCCAAAAAAGGAAATGAGAAATCTGTTAGTACCATTGAGAAATGAT----- 12734
QY 22 GluLeuGlySerGlyIleMetGluLeuThr-----AspThrGluLeuLeuLeuTyr 38
Db 12735 -----ACTCCTCAGAGGAACTCTCAAAATATGTAGACATCATGATTATTGCCCTT 12785
QY 39 ThrArgLysArgAspSerValIleHisTyr-----LeuCysLeuArgArgTyrGly 56
Db 12786 ACTCGAAATCGGAGGACAGGAGATGCTACACTGTGCTCCACTGTGCGGAAACAGTTTAAT 12845
QY 57 TyAspSerAsnLeuPheSerPheGluSerGlyArgCysGlnThrGlyGlnGlyIle 76
Db 12846 GAAAGTCTTACCTCATTTCCACCAG-----AGGACCCACACTCGAGAGAAAA--- 12893
QY 77 PheAlaPheLysCysAlaAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGln 96
Db 12894 ---CCCTATGACTGTAACTACTGTGGGAAAGCTTCAATCATATAAAACAACCTCAATAA 12950
```

```
QY 97 AsnAsnSerIleAsnValValGluGluProVal-----Val 108
Db 12951 CATGACGGAATTCATACAGAGAGAAACCTTATTCCTGTTCTCAGTGTGGAATAAACTTC 13010
QY 109 GluArgAsnAsnHisGlnThrGluLeuGlu 118
Db 13011 CGTCAGAAATCTCATCGGAGTCGTCATGAA 13040

RESULT 14
US-09-248-796A-6449
; Sequence 6449, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6449
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6449
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Alignment Scores:
Pred. No.: 0.386 Length: 1239
Score: 79.00 Matches: 32
Percent Similarity: 43.70% Conservative: 20
Best Local Similarity: 26.89% Mismatches: 47
Query Match: 11.35% Indels: 20
DB: 4 Gaps: 6
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US-09-757-415A-1\_COPY\_11\_140 (1-130) x US-09-248-796A-6449 (1-1239)

```
QY 10 LysPheLysValIleAsnValAspAspGlyAsn-----GluLeuGlySerGlyIle 27
Db 469 AAATTGAAAGTTTCAACGTTAACACATGACACATTCGACATTCGTTTGA 528
QY 28 MetGluLeuThrAspThrGluLeuLeuLeuLeuThrArgLysArgAspSerValIleTyr 47
Db 529 CAAGAAGTCACATGATACATTCGACATTTCTTATTAACGCTGAAAAGGTCGACGTT----- 582
QY 48 HisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe----- 62
Db 583 -----ATTTTGAACAATTTGAGCAGCTGCTAAGAACATTTGTTTACAAACAGTTAAC 633
QY 63 SerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla 82
Db 634 TCATTC---AGTGCTCCAAACCTTGACCATTCGTAACGGTTTCATTTGCTGTTTCATCTTGT 690
QY 83 ArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIleAsnVal 102
Db 691 TCTGTTGAAAAAGTC-----GAACTTGCTGAATTGACTTCTATTGGT--- 732
QY 103 ValGluGluProValValGluArgAsnHisGlnThrGluLeuGluValProArg 121
Db 733 ---AATTCTTACGATATCAACAAAATGATGACTTGACTGAATTAGATTTCCCTNAA 786
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RESULT 15
US-09-023-655-1386
; Sequence 1386, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
```

## TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1386:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5828 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: G386256  
US-09-023-655-1386

## Alignment Scores:

Pred. No.:	5.58	Length:	5828
Score:	78.00	Matches:	21
Percent Similarity:	40.00%	Conservative:	7
Best Local Similarity:	30.00%	Mismatches:	20
Query Match:	11.21%	Indels:	22
DB:	4	Gaps:	1

US-09-757-415A-1\_COPY\_11\_140 (1-130) x US-09-023-655-1386 (1-5828)

QY	52	LeuAtgAtgTyrGlyTyrAspSerAsnLeuPheSerPheGluSerGlyArgArgCysGln	71
Db	1651	ATCAGGCGGTGGGCCAACCTCTTCTTCATCAGGTGGCGGTTCTGCCGTG	1710
QY	72	ThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeu	91
Db	1711	ACGGGGCCCGGGAGTTCTGGATGCAG-----	1737
QY	92	GlnGluIleMetGlnAsnAsnSerIleAsnValValGluGluProValValGluArgAsn	111
Db	1738	-----GTGGATGACTCTGTGGTGGCCAGAAC	1764
QY	112	AsnHisGlnThrGluLeuGluValProArg	121
Db	1765	ATGCACGAGACCATCTCGAGGCCATGCGG	1794

Search completed: February 14, 2005, 03:23:22  
Job time : 232.079 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: February 14, 2005, 03:17:13 ; Search time 715.855 Seconds  
(without alignments)  
1071.529 Million hits updates/sec

Title: US-09-757-415a-1\_COPY\_11\_140  
Perfect score: 696  
Sequence: 1 DTVPDNRNKKFKVINVDDG.....NNHQTELEVPRTPTTGG 130

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 295022984 residues  
Total number of hits satisfying chosen parameters: 10757346  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUPFI=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-FCGPOP=6 -FCGPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	696	100.0	1532	15	US-10-146-473-27	Sequence 27, Appl
2	696	100.0	2074	17	US-10-276-774-842	Sequence 842, App
3	264.5	38.0	452	10	US-09-918-995-27390	Sequence 27390, A
4	143.5	20.6	1908	17	US-10-172-118-601	Sequence 601, App
5	143.5	20.6	1908	17	US-10-342-887-601	Sequence 601, App
6	143.5	20.6	1908	18	US-10-370-715B-49	Sequence 49, Appl
7	143.5	20.6	1972	17	US-10-240-425-380	Sequence 380, App
8	143.5	20.6	3809	13	US-10-001-870-68	Sequence 68, Appl
9	141	20.3	1539	9	US-09-789-919-15	Sequence 15, Appl
10	141	20.3	1850	9	US-09-789-919-57	Sequence 57, Appl
11	137.5	19.8	1146	15	US-10-037-270-854	Sequence 854, App
12	137.5	19.8	1146	17	US-10-117-722-854	Sequence 854, App
13	137.5	19.8	1750	17	US-10-307-928A-5	Sequence 5, Appl
14	135.5	19.5	1221	17	US-10-350-923B-37	Sequence 37, Appl
15	133.5	19.2	914	15	US-10-037-270-855	Sequence 855, App
16	133.5	19.2	914	17	US-10-117-722-855	Sequence 855, App
17	124.5	17.9	1951	13	US-10-098-841-102	Sequence 102, App
18	124.5	17.9	2000	10	US-09-814-353-21341	Sequence 21341, A
19	124.5	17.9	2305	18	US-10-723-860-5489	Sequence 5489, Ap
20	124.5	17.9	2735	15	US-10-037-270-842	Sequence 842, App
21	124.5	17.9	2735	17	US-10-117-722-842	Sequence 842, App
22	122	17.5	421	10	US-09-918-995-34825	Sequence 34825, A
23	120.5	17.3	2339	17	US-10-112-944-41	Sequence 41, Appl
24	113	16.2	508	10	US-09-918-995-24418	Sequence 24418, A
25	111.5	16.0	1385	15	US-10-106-698-1983	Sequence 1983, Ap
26	95.5	13.7	714	16	US-10-029-386-24084	Sequence 24084, A
27	95.5	13.7	804	16	US-10-029-386-24133	Sequence 24133, A
28	95.5	13.7	1409	17	US-10-264-049-165	Sequence 165, App
29	88	12.6	507	16	US-10-029-386-10377	Sequence 10377, A
30	85	12.2	24740	16	US-10-292-951-41	Sequence 41, Appl
31	85	12.2	24740	17	US-10-382-844-41	Sequence 41, Appl
32	83	11.9	1813	14	US-10-114-170-91	Sequence 91, Appl
33	78	11.2	5800	18	US-10-735-512-28	Sequence 28, Appl
34	78	11.2	5828	9	US-09-903-248-6	Sequence 6, Appl
35	78	11.2	5828	9	US-09-859-604-6	Sequence 6, Appl
36	78	11.2	5828	9	US-09-903-063-6	Sequence 6, Appl
37	78	11.2	5828	9	US-09-903-216-6	Sequence 6, Appl
38	78	11.2	5828	9	US-09-903-199-6	Sequence 6, Appl
39	78	11.2	5828	9	US-09-880-107-3021	Sequence 3021, Ap
40	78	11.2	5828	9	US-09-903-023-6	Sequence 6, Appl
41	78	11.2	5828	10	US-09-436-184-6	Sequence 6, Appl
42	78	11.2	5828	17	US-10-172-118-1165	Sequence 1165, Ap
43	78	11.2	5828	17	US-10-342-887-1165	Sequence 1165, Ap
44	78	11.2	5828	17	US-10-641-643-1386	Sequence 1386, Ap
45	78	11.2	6321	17	US-10-334-143-155	Sequence 155, App

ALIGNMENTS

RESULT 1  
US-10-146-473-27  
; Sequence 27, Application US/10146473  
; Publication No. US2003010888A1  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew  
; APPLICANT: Gout, Ivan  
; APPLICANT: Stockert, Elisabeth  
; APPLICANT: Gure, Ali  
; APPLICANT: Chen, Yao-Tseeng  
; APPLICANT: Old, Lloyd  
; TITLE OF INVENTION: Breast Cancer Antigens  
; FILE REFERENCE: L00461/70130(JRV)  
; CURRENT FILING DATE: 2002-05-15  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27

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; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-27

Alignment Scores:
Pred. No.: 1,12e-89 Length: 1532
Score: 696.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-757-415A-1_COPY_11_140 (1-130) x US-10-146-473-27 (1-1532)

QY 1 AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGly 20
   |||||
Db 36 GACACTGTCCCGAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGGG 95

QY 21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 40
   |||||
Db 96 AATGAGTTAGGTTCTGGCATATATGGAACCTTACAGACAGAACTGATTTTATACACCCG 155

QY 41 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
   |||||
Db 156 AAACGTGACTCAGTAAATGGCACTACCTCTGCTGCGACGCTATGGCTATGACTCGAAT 215

QY 61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
   |||||
Db 216 CTCCTTTCTTTTGAAGAGTGGTGGAGGTGTCAAACTGGACAAGGAATCTTTTGCCTTTAAG 275

QY 81 CysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnSerIle 100
   |||||
Db 276 TGTGCCCGTGCAGAGAATTTTAAACATGTTGCAAGAGATTATGCCAAATATATAGTATA 335

QY 101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
   |||||
Db 336 AATGTGGTGGAAAGCCAGTTGTAGAAAGAAATAATCATCAGACAGAAATTGGAAGTCCCT 395

QY 121 ArgThrProArgThrProThrThrProGly 130
   |||||
Db 396 AGAACACCTCGAACACCTCAACTCCAGGA 425

RESULT 2
US-10-276-774-842
; Sequence 842, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 842
; LENGTH: 2074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-842

Alignment Scores:
Pred. No.: 1,76e-89 Length: 2074
Score: 696.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
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US-09-757-415A-1_COPY_11_140 (1-130) x US-10-276-774-842 (1-2074)

QY 1 AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGly 20
   |||||
Db 575 GACACTGTCCCGAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGGG 634

QY 21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 40
   |||||
Db 635 AATGAGTTAGGTTCTGGCATATATGGAACCTTACAGACAGAACTGATTTTATACACCCG 694

QY 41 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
   |||||
Db 695 AAACGTGACTCAGTAAATGGCACTACCTCTGCTGCGACGCTATGGCTATGACTCGAAT 754

QY 61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
   |||||
Db 755 CTCCTTTCTTTTGAAGAGTGGTGGAGGTGTCAAACTGGACAAGGAATCTTTTGCCTTTAAG 814

QY 81 CysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnSerIle 100
   |||||
Db 815 TGTGCCCGTGCAGAGAATTTTAAACATGTTGCAAGAGATTATGCCAAATATATAGTATA 874

QY 101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
   |||||
Db 875 AATGTGGTGGAAAGCCAGTTGTAGAAAGAAATAATCATCAGACAGAAATTGGAAGTCCCT 934

QY 121 ArgThrProArgThrProThrThrProGly 130
   |||||
Db 935 AGAACACCTCGAACACCTACACTCCAGGA 964

RESULT 3
US-09-918-995-27390
; Sequence 27390, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27390
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(452)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27390

Alignment Scores:
Pred. No.: 4,37e-28 Length: 452
Score: 264.50 Matches: 49
Percent Similarity: 84.72% Conservative: 12
Best Local Similarity: 68.06% Mismatches: 10
Query Match: 38.00% Indels: 1
DB: 10 Gaps: 1

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-918-995-27390 (1-452)

QY 60 AsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPhe 79
   |||||
Db 42 CACCTCTTCTCTTTGAGAGTGGCCCGCATGTCCAGACAGCCCATGGATATTTGCATTT 101

QY 80 LysCysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnSer 99
   |||||
Db 102 AAGTGTTCCTCCGGCTGAGGAATCTTCAACCTCTCTCAGGATCTGTGATGCGTCAACAGC 161
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```

; LENGTH: 1972
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF035299
US-10-240-425-380

Alignment Scores:
Pred. No.: 1,24e-09 Length: 1972
Score: 143.50 Matches: 33
Percent Similarity: 47.32% Conservative: 20
Best Local Similarity: 29.46% Mismatches: 50
Query Match: 20.62% Indels: 9
DB: 17 Gaps: 2

US-09-757-415A-1_COPY_11_140 (1-130) x US-10-240-425-380 (1-1972)

QY 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyThrArgLysAsgAsp 43
Db 600 GGCCTCTAGTGTGTGAGGTGGAGCTGAAGGCTGACTCTCTCGACCGTGGGGGCCAG 659
QY 44 Ser-----ValLysTrpHisTyThrLeuCysLeuArgArgTyrgLysTy 57
Db 660 AGTCAGATACTGGAGCCACTCCTCTGCTGGCCCTACACTCTGTGCTGCTATGGCCGG 719
QY 58 AspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePhe 77
Db 720 GACAAAGGTCATGTTCTCTTTTCGAGGCGGCGCGCTGCGCCCTCAGGCGCTTGAACTTC 779
QY 78 AlaPheLysCysAlaAraGluGluLeuPheAsnMetLeuGlnGluMetGlnAsn 97
Db 780 ACCTTCCAGCGGCACAGGAAAGTACATCTTCCAGGCACTTGAGACTGCCATCCACCG 839
QY 98 AsnSerIleAsnValValGlu-----GluProValValGluArgAsnHisGln 114
Db 840 CAGAAGGCCAGGGAAGCGCGAGCGGCACGATGTTCTCAGAGCTGACTCCCATGAA 899
QY 115 ThrGluLeuGluValProArgThrProArgThrPro 126
Db 900 GGGGAGGTGGAGGGAAGTTGCTTCCCACT 935

RESULT 8
US-10-001-870-68
; Sequence 68, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 3809
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-870-68

Alignment Scores:
Pred. No.: 3,33e-09 Length: 3809
Score: 143.50 Matches: 33
Percent Similarity: 47.32% Conservative: 20
Best Local Similarity: 29.46% Mismatches: 50
Query Match: 20.62% Indels: 9
DB: 13 Gaps: 2

```



```
US-09-757-415A-1_COPY_11_140 (1-130) x US-10-001-870-68 (1-3809)
QY 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
Db 2397 GGCTCTACGTCTGGAGGTGGAGGCTGAAAGGCTGACTCTCTGACCGTGGGGGCCAG 2456
QY 44 Ser-----ValIleTyrHisTyrLeuCysLeuArgArgTyrGlyTyr 57
Db 2457 AGTCAGATACTGGAGCCACTCTCTGCTGCGCCCTACACTCTGTGGCTGCTATGGCCGG 2516
QY 58 AspSerAsnLeuPheSerPheGluSerGlyArgCysGlnThrGlyGlnGlyIlePhe 77
Db 2517 GACAGGTCTATGTTCTTCTTCGAGCGCGCGCGCTGCCCTCAGCGCCCTGGAACCTTC 2576
QY 78 AlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluLeuMetGlnAsn 97
Db 2577 ACCTTCAGACGGCACAGGGAATGATCATCTTCAGGCAGTTGAGACTGCCACCCGG 2636
QY 98 AsnSerIleAsnValValGlu-----GluProValValGluArgAsnAsnHisGln 114
Db 2637 CAGAGGCCCGAGGAAGCGCGACAGGGGCACAGATGTTCTCAGAGCTGACTCCCATGAA 2696
QY 115 ThrGluLeuGluValProArgThrProArgThrPro 126
Db 2697 GGGGAGGTGGCAGAGGGGAAGTTGCCCTTCCCCACCT 2732

RESULT 9
US-09-789-919-15
; Sequence 15, Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor
; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; FILE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789, 919
; CURRENT FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-789-919-15
Alignment Scores:
Pred. No.: 1,97e-09 Length: 1539
Score: 141.00 Matches: 36
Percent Similarity: 44.09% Conservative: 20
Best Local Similarity: 28.35% Mismatches: 47
Query Match: 20.26% Indels: 24
DB: Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-789-919-15 (1-1539)
QY 23 LeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArg 42
Db 560 CTGGGCCAAGATGACATCCAACTGAGGGAGACA-----TCCAGAGCCCGAG 604
QY 43 AspSerValIleTyrHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe 62
Db 605 GCCTGTTTAGTGGCCCTACCGTTTCTCGCAAGTACGGCTCTGACAAGGGGTGTGTTTC 664
QY 63 SerPheGluSerGlyArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla 82
Db 665 TCGTTTGGAGTGGCGCGCTGTGACTCAGGTGAGGGCTTTTTCCTTCAGTAGCCCG 724
QY 83 ArgAlaGluLeuPheAsnMetLeuGlnGluLeuMetGlnAsnSerIleAsnVal 102
Db 725 CGTGCCCCAGACATATGTGGGTGTGGCTGCGCCCATTTGCCCGCCAGCGGAGCGTCT 784
QY 103 ValGlu----- 104

US-09-789-919-15
Alignment Scores:
Pred. No.: 1,97e-09 Length: 1539
Score: 141.00 Matches: 36
Percent Similarity: 44.09% Conservative: 20
Best Local Similarity: 28.35% Mismatches: 47
Query Match: 20.26% Indels: 24
DB: Gaps: 3

US-09-757-415A-1_COPY_11_140 (1-130) x US-09-789-919-57 (1-1650)
QY 23 LeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArg 42
Db 671 CTGGGCCAAGATGACATCCAACTGAGGGAGACA-----TCCAGAGCCCGAG 715
QY 43 AspSerValIleTyrHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe 62
Db 716 GCCTGTTTAGTGGCCCTACCGTTTCTCGCAAGTACGGCTCTGACAAGGGGTGTGTTTC 775
QY 63 SerPheGluSerGlyArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla 82
Db 776 TCGTTTGGAGTGGCGCGCTGTGACTCAGGTGAGGGCTTTTTCCTTCAGTAGCCCG 835
QY 83 ArgAlaGluLeuPheAsnMetLeuGlnGluLeuMetGlnAsnSerIleAsnVal 102
Db 836 CGTGCCCCAGACATATGTGGGTGTGGCTGCGCCCATTTGCCCGCCAGCGGAGCGTCT 895
QY 103 ValGlu----- 104
Db 896 CCAGAGCTGGCCATGTCACCCCTGCCCTCGCGGCCCTCTCCCTGCCCTCCCTA 955
QY 105 GluProValValGluArgAsnAsnHisGlnThrGluLeuGluValProArgThrProArg 124
Db 956 GAGCCCCCTGGAGAGCTTCGGGAGGTGGGCCCCAGGATTTGAGCTGCCCACTCCCGAAAG 1015
QY 125 ThrPro---ThrThrProGly 130
Db 1016 CTGGCTCTAACTGATCCCGGG 1036

RESULT 11
US-10-037-270-854
; Sequence 854, Application US/10037270
; Publication No. US20030104529A1
```



APPLICANT: Burgess, Catherine E.  
APPLICANT: Catterton, Elina  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Ji, Weizhen  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: Patturajan, Meera  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A.M.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zhong, Mei  
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF  
; Publication No. US2004002084A1  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Ma, Xiao Jun  
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from active  
; FILE REFERENCE: S03157-01  
; CURRENT APPLICATION NUMBER: US/10/307,928A  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: 60/381,495  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/383,744  
; PRIOR FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: 60/384,024  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: 60/401,788  
; PRIOR FILING DATE: 2002-08-07  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Curaseqdist version 0.1  
; SEQ ID NO 5  
; LENGTH: 1750  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (197)..(1189)  
US-10-307-928A-5  
Alignment Scores:  
Pred. No.: 7 64e-09 Length: 1750  
Score: 137.50 Matches: 34  
Percent Similarity: 49.07% Conservative: 19  
Best Local Similarity: 31.48% Mismatches: 42  
Query Match: 19.76% Indels: 13  
DB: 17 Gaps: 3  
US-09-757-415A-1\_COPY\_11\_140 (1-130) x US-10-307-928A-5 (1-1750)  
QY 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43  
Db 653 GGTGATGCACATGCAGATCATGAAATATCTATCTCGGATATCCCAATGCC 712  
QY 44 SerValLys-----TrpHisTyrLeuCysLeuArgGlyTyrAspSerAsn 60  
Db 713 AAGGTCAAATGGTGTGTGGCCCTCTCAGTCACTGAGGAGATACGGTCGGGACTCAAG 772  
QY 61 LeuPheSerPheGluSerGlyArgGlyCysGlnThrGlyGlnGlyIlePheAlaPheLys 80  
Db 773 TGGTTCACGTTTGAGTCAGGAAGATGTGTGACACAGGAGGAGGACTATCTACTTTTCAA 932

QY 81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluMetLeuGlnAsnSerIle 100  
Db 833 ACAAGGGAAGAGAA-----ATGATCTATCAGAAGGTTTCATTCTGGGACACTG 880  
QY 101 AsnValValGluGlu-----ProValValGluArgAsnAsnHisGln 114  
Db 881 GCCATAGCTGAGCAACATGAAGATTAACTAGTAATGAACAGAGGCCCGCTTCAG 940  
QY 115 ThrGluLeuGluValProArgThr 122  
Db 941 ACAAGCTTGACTGAACCAATGACA 964

## RESULT 14

US-10-350-923B-37  
; Sequence 37, Application US/10350923B  
; Publication No. US2004002084A1  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Ma, Xiao Jun  
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from active  
; FILE REFERENCE: S03157-01  
; CURRENT APPLICATION NUMBER: US/10/350,923B  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: US/ 09/454,280  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: PCT/US99/28773  
; PRIOR FILING DATE: 1999-06-12  
; PRIOR APPLICATION NUMBER: US 60/111,006  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 37  
; LENGTH: 1221  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-350-923B-37

## Alignment Scores:

Pred. No.: 8 67e-09 Length: 1221  
Score: 135.50 Matches: 37  
Percent Similarity: 49.07% Conservative: 16  
Best Local Similarity: 34.26% Mismatches: 35  
Query Match: 19.47% Indels: 20  
DB: 17 Gaps: 4

US-09-757-415A-1\_COPY\_11\_140 (1-130) x US-10-350-923B-37 (1-1221)

QY 38 TyrThrArgLysArgAsp---SerValLys-TrpHisTyrLeuCysLeuArgGlyTyrGln 56  
Db 348 TGGGCCCGAGCCAGGAGCCAGCTGTACGCTGGCCCTACAGGTTTCTCGCGGCTTTGG 407  
QY 56 TyrAspSerAsnLeuPheSerPheGluSerGlyArgGlyCysGlnThrGlyGlnGlyIle 76  
Db 408 GCGGACAAAGGTAACTCTTTCTTTGAGCGAGCGCGCTGCTGCTCTGGAGAGGGCAA 467  
QY 76 ePheAlaPheLysCysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMet-- 95  
Db 468 CTTTGAGTTTGAACCCCGGCAAGGCAATGAGATCTTTTGGCCCTTGAAGAGGCCATCTC 527  
QY 96 ----GlnAsnAsnSerIleAsnValValGluGluProValValGluArgAsnAsnHisGln 114  
Db 528 TGCCCAAGAAGATGCTGACCCGCTACACCCCAACCG-----CAGCCAGCCAC 575  
QY 114 nThrGluLeuGluValProArg-----Th 122  
Db 576 AATCCCGCGTCCGTCGCCCCCGCCCTAGTACCCCTACTCTCGGCCGCGATGACTACTGCC 635  
QY 122 rProArgThrProThrThrPro 129  
Db 636 GCGGCTTCACCCACCACACACCG 657

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Db      835 CAGAGCGCGGTAAAGGCCCTTCT 861      ::: ||| |||
Search completed: February 14, 2005, 05:17:58
Job time : 827.855 secs

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RESULT 15
US-10-037-270-855
/ Sequence 855, Application US/10037270
/ Publication No. US20030104529A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-bong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunding
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Tillinghast, John
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. US20030104529A1elel Nucleic Acids and
/ FILE OF INVENTION: Polypeptides
/ FILE REFERENCE: 784CIP28
/ CURRENT APPLICATION NUMBER: US/10/037,270
/ CURRENT FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1104
/ SOFTWARE: pt_FL_genes Version 1.0
/ SEQ ID NO 855
/ LENGTH: 914
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (109)..(867)
US-10-037-270-855

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Alignment Scores:					
Pred. No.:	1..09e-08	Length:	914		
Score:	133.50	Matches:	33		
Percent Similarity:	48.62%	Conservative:	20		
Best Local Similarity:	30.28%	Mismatches:	43		
Query Match:	19.18%	Indels:	13		
DB:	15	Gaps:	3		
US-09-757-415A-1_COPY_11_140 (1-130) x US-10-037-270-855 (1-914)					
QY	24	GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyThrArgLysAlaGsp	43		
Db	565	GGTGAATGCACAAATGCAGATCACTCATCAAATAATCTATCTCTGGGATATCCCAATGCC	524		
QY	44	SerVallys-----TriHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAan	60		
Db	625	AAGGTCAAACACTGGTGTCCTCTCAGCTCACTGAGGAGATACGGTCGGAGCTCAACG	684		
QY	61	LeuPheSerPheGluSerGlyVargArgCysGlnThrGlyGlnGlyIlePheAlaPheLys	80		
Db	685	TGGTTCCACGTTTTGAGTCAGGAAGAATGTGTGACACAGAGAACGACTATTTCACCTTTTCAA	744		
QY	81	CysAlaAargAlaGluGluLeuPheAsnMetLeuGlnLuileMetGlnAasnAasnSeriIle	100		
Db	745	ACAAGGGAAGGAGAA-----ATGATCTATCAGAAGGTTCATCTTCGCACACTG	792		
QY	101	AasnValvalGluCluProvalValGluIargAasnHnsGlnThrGluLeuGluIalPro	120		
Db	793	GCATATAGCTGACGCAA-----CATGAAGATTTAATGCTAGAAAATGGAA	834		
QY	121	ArgThrProArgThrProThrThrPro	129		

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 14, 2005, 02:44:53 ; Search time 5.06579 Seconds  
(without alignments)  
324.190 Million cell updates/sec

Title: US-09-757-415a-3

Perfect score: 107

Sequence: 1 HSQMAVHKLAKSIPLRRQVTVS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	729	1	US-07-640-029-3
2	107	100.0	731	1	US-07-921-807B-5
3	107	100.0	731	1	US-08-441-944A-5
4	107	100.0	731	3	US-08-439-992A-3
5	107	100.0	733	1	US-07-640-029-4
6	107	100.0	733	1	US-07-921-807B-6
7	107	100.0	733	1	US-08-441-944A-6
8	107	100.0	733	1	US-08-439-992A-4
9	107	100.0	816	1	US-07-640-029-1
10	107	100.0	817	1	US-07-640-029-2
11	107	100.0	820	1	US-07-921-807B-3
12	107	100.0	820	1	US-08-441-944A-3
13	107	100.0	820	1	US-08-166-717D-6
14	107	100.0	820	3	US-08-439-992A-1
15	107	100.0	822	1	US-07-997-133-1
16	107	100.0	822	1	US-07-921-807B-4
17	107	100.0	822	1	US-08-459-296-2
18	107	100.0	822	1	US-08-441-944A-4
19	107	100.0	822	2	US-08-451-822A-12
20	107	100.0	822	3	US-08-439-992A-2
21	107	100.0	822	3	US-08-323-430-12
22	101	94.4	609	4	US-09-949-016-7747
23	101	94.4	609	4	US-09-949-016-7748
24	101	94.4	609	4	US-09-949-016-7749
25	101	94.4	609	4	US-09-949-016-7750
26	101	94.4	609	4	US-09-949-016-7751
27	101	94.4	609	4	US-09-949-016-7752

28	101	94.4	609	4	US-09-949-016-7753	Sequence 7753, Ap
29	101	94.4	609	4	US-09-949-016-7754	Sequence 7754, Ap
30	83	77.6	643	1	US-08-471-570-6	Sequence 6, Appli
31	83	77.6	769	1	US-08-471-570-8	Sequence 8, Appli
32	83	77.6	821	2	US-08-451-822A-13	Sequence 13, Appli
33	83	77.6	821	3	US-08-323-430-13	Sequence 13, Appli
34	81	75.7	729	1	US-08-070-165F-6	Sequence 6, Appli
35	81	75.7	729	2	US-08-885-418-6	Sequence 6, Appli
36	81	75.7	731	1	US-08-070-165F-10	Sequence 10, Appli
37	81	75.7	731	2	US-08-885-418-10	Sequence 10, Appli
38	77	72.0	471	4	US-09-949-016-9042	Sequence 9042, Ap
39	77	72.0	471	4	US-09-949-016-9043	Sequence 9043, Ap
40	77	72.0	471	4	US-09-949-016-9044	Sequence 9044, Ap
41	77	72.0	471	4	US-09-949-016-9045	Sequence 9045, Ap
42	77	72.0	471	4	US-09-949-016-9046	Sequence 9046, Ap
43	77	72.0	471	4	US-09-949-016-9047	Sequence 9047, Ap
44	77	72.0	471	4	US-09-949-016-9048	Sequence 9048, Ap
45	77	72.0	471	4	US-09-949-016-9049	Sequence 9049, Ap

## ALIGNMENTS

RESULT 1

US-07-640-029-3

; Sequence 3, Application US/07640029

; Patent No. 5229501

; GENERAL INFORMATION:

; APPLICANT: Kiefer, Michael C.

; APPLICANT: Valenzuela, Pablo D.T.

; APPLICANT: Barr, Philip J.

; TITLE OF INVENTION: Expression and Use of Human Fibroblast

; TITLE OF INVENTION: Growth Factor Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: California

; COUNTRY: USA

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/640,029

; FILING DATE: 19910111

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: McClung, Barbara G.

; REGISTRATION NUMBER: 33,113

; REFERENCE/DOCKET NUMBER: CH-165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 510-601-2708

; TELEFAX: 510-655-3542

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 729 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-640-029-3

Query Match 100.0%; Score 107; DB 1; Length 729;

Best Local Similarity 100.0%; Pred. No. 1.3e-09;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRRQVTVS 22

Db 316 HSQMAVHKLAKSIPLRRQVTVS 337

RESULT 2  
US-07-921-807B-5  
; Sequence 5, Application US/07921807B  
; Patent No. 5474914  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; TITLE OF INVENTION: OF VIRAL PROTEINS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 29-SEP-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209.001  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 731 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-921-807B-5

Query Match 100.0%; Score 107; DB 1; Length 731;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22  
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DB 318 HSQMAVHKLAKSIPLRRQVTVS 339

RESULT 3  
US-08-441-944A-5  
; Sequence 5, Application US/08441944A  
; Patent No. 5767250  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; TITLE OF INVENTION: OF VIRAL PROTEINS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,944A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/921,807  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209.001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 731 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-441-944A-5

Query Match 100.0%; Score 107; DB 1; Length 731;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22  
|||  
DB 318 HSQMAVHKLAKSIPLRRQVTVS 339

RESULT 4  
US-08-439-992A-3  
; Sequence 3, Application US/08439992A  
; Patent No. 6255454  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Pablo, Valenzuela D.T.  
; APPLICANT: Philip, Barry J.  
; TITLE OF INVENTION: Expression and Use of Human Fibroblast  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,992A  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chung, Ling-Fong  
; REGISTRATION NUMBER: 36,482  
; REFERENCE/DOCKET NUMBER: 0165.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-923-2704  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 731 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-439-992A-3

Query Match 100.0%; Score 107; DB 3; Length 731;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSOQAVHKLAKSIPLRRQVTVS 22  
318 HSOQAVHKLAKSIPLRRQVTVS 339

RESULT 5

US-07-640-029-4

; Sequence 4, Application US/07640029  
; Patent No. 5229501  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Valenzuela, Pablo D.T.  
; APPLICANT: Bart, Philip J.  
; TITLE OF INVENTION: Expression and Use of Human Fibroblast  
; TITLE OF INVENTION: Growth Factor Receptor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/640,029  
; FILING DATE: 19910111  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McClung, Barbara G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: CH-165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-601-2708  
; TELEFAX: 510-655-3542  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 733 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-640-029-4

Query Match 100.0%; Score 107; DB 1; Length 733;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSOQAVHKLAKSIPLRRQVTVS 22  
320 HSOQAVHKLAKSIPLRRQVTVS 341

RESULT 6

US-07-921-807B-6

; Sequence 6, Application US/07921807B  
; Patent No. 547914  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; TITLE OF INVENTION: OF VIRAL PROTEINS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/921,807B  
; FILING DATE: 29-SEP-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209.001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 733 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-921-807B-6

Query Match 100.0%; Score 107; DB 1; Length 733;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSOQAVHKLAKSIPLRRQVTVS 22  
320 HSOQAVHKLAKSIPLRRQVTVS 341

RESULT 7

US-08-441-944A-6

; Sequence 6, Application US/08441944A  
; Patent No. 5767250  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; TITLE OF INVENTION: OF VIRAL PROTEINS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,944A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/921,807  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209.001  
; TELECOMMUNICATION INFORMATION:

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/ TELEPHONE: (510) 601-2708
/ TELEFAX: (510) 655-3542
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 733 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
US-08-441-944A-6

Query Match      100.0%; Score 107; DB 1; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 320 HSQMAVHKLAKSIPLRRQVTVS 341

RESULT 8
US-08-439-992A-4
/ Sequence 4, Application US/08439992A
/ Patent No. 6255454
/ GENERAL INFORMATION:
/   APPLICANT: Kiefer, Michael C.
/   APPLICANT: Pablo, Valenzuela D.T.
/   APPLICANT: Philip, Barr J.
/   TITLE OF INVENTION: Expression and Use of Human Fibroblast
/   NUMBER OF SEQUENCES: 12
/   CORRESPONDENCE ADDRESS:
/     ADDRESSEE: Chiron Corporation
/     STREET: 4560 Horton Street
/     CITY: Emeryville
/     STATE: CA
/     COUNTRY: USA
/     ZIP: 94608
/   COMPUTER READABLE FORM:
/     MEDIUM TYPE: Floppy disk
/     OPERATING SYSTEM: PC-DOS/MS-DOS
/     SOFTWARE: Patent In Release #1.0, Version #1.30
/     CURRENT APPLICATION DATA:
/       APPLICATION NUMBER: US/08/439,992A
/       FILING DATE: 12-MAY-1995
/     CLASSIFICATION: 530
/     ATTORNEY/AGENT INFORMATION:
/       NAME: Chung, Ling-Fong
/       REGISTRATION NUMBER: 36,482
/       REFERENCE/DOCKET NUMBER: 0165.004
/     TELECOMMUNICATION INFORMATION:
/       TELEPHONE: 510-923-2704
/       TELEFAX: (510) 655-3542
/     INFORMATION FOR SEQ ID NO: 4:
/       SEQUENCE CHARACTERISTICS:
/         LENGTH: 733 amino acids
/         TYPE: amino acid
/         STRANDEDNESS: single
/         TOPOLOGY: linear
/         MOLECULE TYPE: protein
US-08-439-992A-4

Query Match      100.0%; Score 107; DB 3; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 320 HSQMAVHKLAKSIPLRRQVTVS 341

RESULT 9
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US-07-640-029-1
/ Sequence 1, Application US/07640029
/ Patent No. 5229501
/ GENERAL INFORMATION:
/   APPLICANT: Kiefer, Michael C.
/   APPLICANT: Valenzuela, Pablo D.T.
/   APPLICANT: Barr, Philip J.
/   TITLE OF INVENTION: Expression and Use of Human Fibroblast
/   NUMBER OF SEQUENCES: 12
/   CORRESPONDENCE ADDRESS:
/     ADDRESSEE: Chiron Corporation
/     STREET: 4560 Horton Street
/     CITY: Emeryville
/     STATE: California
/     COUNTRY: USA
/     ZIP: 94608
/   COMPUTER READABLE FORM:
/     MEDIUM TYPE: Floppy disk
/     OPERATING SYSTEM: PC-DOS/MS-DOS
/     SOFTWARE: Patent In Release #1.0, Version #1.25
/     CURRENT APPLICATION DATA:
/       APPLICATION NUMBER: US/07/640,029
/       FILING DATE: 19910111
/     CLASSIFICATION: 530
/     ATTORNEY/AGENT INFORMATION:
/       NAME: Mcclung, Barbara G.
/       REGISTRATION NUMBER: 33,113
/       REFERENCE/DOCKET NUMBER: CH-165
/     TELECOMMUNICATION INFORMATION:
/       TELEPHONE: 510-601-2708
/       TELEFAX: 510-655-3542
/     INFORMATION FOR SEQ ID NO: 1:
/       SEQUENCE CHARACTERISTICS:
/         LENGTH: 816 amino acids
/         TYPE: AMINO ACID
/         STRANDEDNESS: single
/         TOPOLOGY: linear
/         MOLECULE TYPE: peptide
US-07-640-029-1

Query Match      100.0%; Score 107; DB 1; Length 816;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
DB 404 HSQMAVHKLAKSIPLRRQVTVS 425

RESULT 10
US-07-640-029-2
/ Sequence 2, Application US/07640029
/ Patent No. 5229501
/ GENERAL INFORMATION:
/   APPLICANT: Kiefer, Michael C.
/   APPLICANT: Valenzuela, Pablo D.T.
/   APPLICANT: Barr, Philip J.
/   TITLE OF INVENTION: Expression and Use of Human Fibroblast
/   NUMBER OF SEQUENCES: 12
/   CORRESPONDENCE ADDRESS:
/     ADDRESSEE: Chiron Corporation
/     STREET: 4560 Horton Street
/     CITY: Emeryville
/     STATE: California
/     COUNTRY: USA
/     ZIP: 94608
/   COMPUTER READABLE FORM:
/     MEDIUM TYPE: Floppy disk
/     OPERATING SYSTEM: PC-DOS/MS-DOS
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;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA: US/07/640,029  
;; APPLICATION NUMBER: 530  
;; FILING DATE: 19910111  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McClung, Barbara G.  
;; REGISTRATION NUMBER: 33,113  
;; REFERENCE/DOCKET NUMBER: CH-165  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 510-601-2708  
;; TELEFAX: 510-655-3542  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 817 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-07-640-029-2

Query Match 100.0%; Score 107; DB 1; Length 817;  
Best Local Similarity 100.0%; Pred. No. 1.4e-09;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRRQTVS 22  
Db 409 HSQMAVHKLAKSIPLRRQTVS 430

RESULT 11  
US-07-921-807B-3  
; Sequence 3, Application US/07921807B  
; Patent No. 5474914  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/921,807B  
; FILING DATE: 29-SEP-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209.001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 820 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-921-807B-3

Query Match 100.0%; Score 107; DB 1; Length 820;  
Best Local Similarity 100.0%; Pred. No. 1.4e-09;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HSQMAVHKLAKSIPLRRQTVS 22  
Db 407 HSQMAVHKLAKSIPLRRQTVS 428

RESULT 12  
US-08-441-944A-3  
; Sequence 3, Application US/08441944A  
; Patent No. 5767250  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,944A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/921,807  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209.001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 820 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-441-944A-3

Query Match 100.0%; Score 107; DB 1; Length 820;  
Best Local Similarity 100.0%; Pred. No. 1.4e-09;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRRQTVS 22  
Db 407 HSQMAVHKLAKSIPLRRQTVS 428

RESULT 13  
US-08-166-717D-6  
; Sequence 6, Application US/08166717D  
; Patent No. 5789182  
; GENERAL INFORMATION:  
; APPLICANT: YAYON, AVNER  
; APPLICANT: ORNITZ, DAVID M.  
; APPLICANT: KLASBRUN, MICHAEL  
; APPLICANT: LEDER, PHILIP  
; TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING  
; TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH  
; FACTOR RECEPTOR  
; NUMBER OF SEQUENCES: 6

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,717D
; FILING DATE: 12/14/93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/631,717
; FILING DATE: 12/20/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Kristina Bieker-Brady
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 00383/017002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-4123
; TELEFAX: (617) 723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 820
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-166-717D-6

Query Match 100.0%; Score 107; DB 1; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 407 HSQMAVHKLAKSIPLRRQVTVS 428

RESULT 14
US-08-439-992A-1
; Sequence 1, Application US/08439992A
; Patent No. 6255454
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Pablo, Valenzuela D.T.
; TITLE OF INVENTION: Expression and Use of Human Fibroblast
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,992A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Pong

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,717D
; FILING DATE: 12/14/93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/631,717
; FILING DATE: 12/20/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Kristina Bieker-Brady
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 00383/017002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-4123
; TELEFAX: (617) 723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 820
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-166-717D-6

Query Match 100.0%; Score 107; DB 1; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 407 HSQMAVHKLAKSIPLRRQVTVS 428

RESULT 15
US-07-997-133-1
; Sequence 1, Application US/07997133
; Patent No. 5288855
; GENERAL INFORMATION:
; APPLICANT: Bergonzoni, Laura
; APPLICANT: Mazue, Guy
; APPLICANT: Isacchi, Antonella
; APPLICANT: Roncucci, Romeo
; APPLICANT: Sarmientos, Paolo
; TITLE OF INVENTION: Extracellular Form of the Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/997,133
; FILING DATE: 28-DEC-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,755
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5288855man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-226-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-4500
; TELEFAX: (703) 486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-997-133-1

Query Match 100.0%; Score 107; DB 1; Length 822;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSQMAVHKLAKSIPLRQVTVS 22

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Db 409 HSQMAVHKLAKSIPLRQVTVS 430

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Job time : 5.06579 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 03:10:48 ; Search time 13.3158 Seconds  
(without alignments)  
539.846 Million cell updates/sec

Title: US-09-757-415A-3

Perfect score: 107  
Sequence: 1 HSQMAVHKLAKSIPLRRQVTVS 22

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Searched: 1376875 seqs, 326749119 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

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20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARTES

Result No.	Score	Query Match	Length	DB	ID	Description
1	107	100.0	22	10	US-09-757-415A-3	Sequence 3, Appli
2	107	100.0	702	9	US-09-805-020-47	Sequence 47, Appl
3	107	100.0	735	15	US-10-307-817-6	Sequence 6, Appli
4	107	100.0	764	9	US-09-925-302-714	Sequence 714, App
5	107	100.0	764	10	US-09-925-302-714	Sequence 714, App
6	107	100.0	820	15	US-10-302-812-42	Sequence 42, Appl
7	107	100.0	822	10	US-09-757-415A-2	Sequence 2, Appli
8	107	100.0	822	14	US-10-204-041-2	Sequence 2, Appli
9	107	100.0	822	15	US-10-394-322A-26	Sequence 26, Appl
10	107	100.0	822	15	US-10-307-817-8	Sequence 8, Appli
11	107	100.0	824	15	US-10-307-817-4	Sequence 4, Appli
12	101	94.4	451	13	US-10-087-192-381	Sequence 381, App
13	101	94.4	609	13	US-10-087-192-384	Sequence 384, App

14	83	77	6	821	15	US-10-394-322A-27	Sequence 27, App1
15	83	77	6	821	15	US-10-302-812-44	Sequence 44, App1
16	83	77	6	822	16	US-10-648-593-254	Sequence 254, App
17	77	52	0	471	13	US-10-087-182-1134	Sequence 1134, App
18	64	59	8	20	14	US-10-099-890-2137	Sequence 2137, App
19	47	43	9	3588	16	US-10-741-601-378	Sequence 378, App
20	47	43	9	3588	17	US-10-741-600-1104	Sequence 1104, App
21	47	43	9	4346	16	US-10-741-601-377	Sequence 377, App
22	47	43	9	4346	17	US-10-741-600-1103	Sequence 1103, App
23	47	43	9	4347	16	US-10-741-601-376	Sequence 376, App
24	47	43	9	4347	17	US-10-741-600-1102	Sequence 1102, App
25	47	43	9	4370	16	US-10-408-765A-1267	Sequence 1267, App
26	47	43	9	4393	15	US-10-231-956A-366	Sequence 366, App
27	47	43	9	4393	17	US-10-741-600-1105	Sequence 1105, App
28	44	41	1	63	16	US-10-437-963-145357	Sequence 145357, App
29	44	41	1	95	15	US-10-424-593-227789	Sequence 227789, App
30	44	41	1	194	9	US-09-738-626-3731	Sequence 3731, App
31	44	41	1	214	15	US-10-424-599-227795	Sequence 227795, App
32	44	41	1	234	15	US-10-424-599-227788	Sequence 227788, App
33	44	41	1	1520	14	US-10-017-161-718	Sequence 718, App
34	44	41	1	1520	15	US-10-292-798-630	Sequence 630, App
35	43	40	7	60	16	US-10-437-963-115591	Sequence 115591, App
36	43	40	2	40	15	US-10-424-593-203535	Sequence 203535, App
37	43	40	2	152	15	US-10-424-599-150884	Sequence 150884, App
38	43	40	2	152	16	US-10-437-963-116361	Sequence 116361, App
39	43	40	2	155	16	US-10-767-701-58588	Sequence 58588, App
40	43	40	2	207	16	US-10-437-963-155843	Sequence 155843, App
41	43	40	2	277	15	US-10-282-122A-5737	Sequence 5737, App
42	43	40	2	277	15	US-10-358-448A-8	Sequence 8, App1
43	43	40	2	339	15	US-10-369-493-16476	Sequence 16476, App
44	43	40	2	446	15	US-10-282-122A-77108	Sequence 77108, App
45	43	40	2	778	16	US-10-437-963-118289	Sequence 118289, App

## ALIGNMENTS

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RESULT 1
US-09-757-415A-3
; Sequence 3, Application US/09757415A
; Publication No. US20030040612A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
; FILE REFERENCE: 2459-1-002N
; CURRENT APPLICATION NUMBER: US/09/757,415A
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-757-415A-3

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Query Match      100.0%; Score 107; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 HSQMAVHKLAKSIPLRQVTVS 22  
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Dh 1 HSQMAVHKLAKSIPLRQVTVS 22

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RESULT 2
US-09-805-020-47
; Sequence 47, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES

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; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-020-47

Query Match      100.0%; Score 107; DB 9; Length 702;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 409 HSQMAVHKLAKSIPLRRQVTVS 430

RESULT 3
US-10-307-817-6
; Sequence 6, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 6
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-6

Query Match      100.0%; Score 107; DB 15; Length 735;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 322 HSQMAVHKLAKSIPLRRQVTVS 343

RESULT 4
US-09-925-302-714
; Sequence 714, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 714
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-714

Query Match      100.0%; Score 107; DB 9; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 351 HSQMAVHKLAKSIPLRRQVTVS 372

RESULT 5
US-09-925-302-714
; Sequence 714, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 714
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-714

Query Match      100.0%; Score 107; DB 9; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 351 HSQMAVHKLAKSIPLRRQVTVS 372

RESULT 6
US-10-302-812-42
; Sequence 42, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 6
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-42

Query Match      100.0%; Score 107; DB 10; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSQMAVHKLAKSIPLRRQVTVS 22
Db 351 HSQMAVHKLAKSIPLRRQVTVS 372
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; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND
; FILE OF INVENTION: TISSUE REGENERATION
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-42

Query Match      100.0%; Score 107; DB 15; Length 820;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRQVTVS 428

RESULT 7
US-09-757-415A-2
; Sequence 2, Application US/09757415A
; Publication No. US20030040612A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
; FILE REFERENCE: 2459-1-002N
; CURRENT APPLICATION NUMBER: US/09/757,415A
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-757-415A-2

Query Match      100.0%; Score 107; DB 10; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRQVTVS 430

RESULT 8
US-10-204-041-2
; Sequence 2, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
; APPLICANT: STEIN-GERLACH, MATTHIAS
; APPLICANT: SALASSIDIS, KONSTADINOS
; APPLICANT: BACHER, GERALD
; APPLICANT: MULLER, STEFAN
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion
; FILE OF INVENTION: Infections and Prion Diseases
; FILE REFERENCE: AXM-007.1P US
; CURRENT APPLICATION NUMBER: US/10/204,041
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: EP 0111858.5
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/EP02/05420
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-204-041-2

Query Match      100.0%; Score 107; DB 14; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRQVTVS 430

RESULT 9
US-10-394-322A-26
; Sequence 26, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-26

Query Match      100.0%; Score 107; DB 15; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRQVTVS 430

RESULT 10
US-10-307-817-8
; Sequence 8, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 8
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-8

Query Match      100.0%; Score 107; DB 15; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSQMAVHKLAKSIPLRQVTVS 22
Db      409 HSQMAVHKLAKSIPLRQVTVS 430

RESULT 11
US-10-307-817-4
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; Sequence 4, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-4

Query Match      100.0%; Score 107; DB 15; Length 824;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HSO MAVHKLAKSIPLRRQVTVS 22
Db      411 HSO MAVHKLAKSIPLRRQVTVS 432

RESULT 12
US-10-087-192-381
; Sequence 381, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 381
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-381

Query Match      94.4%; Score 101; DB 13; Length 451;
Best Local Similarity 95.5%; Pred. No. 1.5e-08;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 HSO MAVHKLAKSIPLRRQVTVS 22
Db      428 HSO MAVHKLAKSIPLRRQVTVS 449

RESULT 13
US-10-087-192-384
; Sequence 384, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586

; Sequence 4, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-4

Query Match      94.4%; Score 101; DB 13; Length 609;
Best Local Similarity 95.5%; Pred. No. 2.1e-08;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 HSO MAVHKLAKSIPLRRQVTVS 22
Db      586 HSO MAVHKLAKSIPLRRQVTES 607

RESULT 14
US-10-394-322A-27
; Sequence 27, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-27

Query Match      77.6%; Score 83; DB 15; Length 821;
Best Local Similarity 85.7%; Pred. No. 3.5e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 SQA VHKLAKSIPLRRQVTVS 22
Db      411 SQA VHKLTKRIPLRQVTVS 431

RESULT 15
US-10-302-812-44
; Sequence 44, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-44

Query Match      77.6%; Score 83; DB 15; Length 821;
Best Local Similarity 85.7%; Pred. No. 3.5e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 SQA VHKLAKSIPLRRQVTVS 22
Db      411 SQA VHKLTKRIPLRQVTVS 431
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Db 411 SQPAVHKLTKRIPLRQVTVS 431

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2005, 03:11:53 ; Search time 37.9211 Seconds  
(without alignments)  
949.290 Million cell updates/sec

Title: US-09-757-415A-3

Perfect score: 107

Sequence: 1 HSQMAVHLAKSLPLRRQVTVS 22

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Ygapop 10.0			0.5
Fgapop 6.0			7.0
Delop 6.0			7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09757415@cgm2\_1\_93 @runat\_07022005\_160041\_26836 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*

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- 4: /cgm2\_6/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cgm2\_6/ptodata/1/ina/PTCUS.COMB.seq:\*
- 6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107	100.0	2360	4	US-09-023-655-1288
2	107	100.0	2469	1	US-07-997-133-2
3	107	100.0	2469	1	US-08-459-296-1
4	107	100.0	2469	5	US-07-997-133-2
5	107	100.0	2662	2	US-08-451-822A-14
6	107	100.0	2662	3	US-08-323-430-14
7	107	100.0	2733	1	US-08-371-001-14
8	107	100.0	2733	5	US-08-459-296-1
9	107	100.0	3503	1	US-07-631-717A-1
10	107	100.0	3503	1	US-08-166-717D-1
11	101	94.4	3944	4	US-09-949-016-1876
12	101	94.4	3944	4	US-09-949-016-1877

13	101	94.4	3944	4	US-09-949-016-1878	Sequence 1878, Ap
14	101	94.4	3944	4	US-09-949-016-1879	Sequence 1879, Ap
15	101	94.4	3944	4	US-09-949-016-1880	Sequence 1880, Ap
16	101	94.4	3944	4	US-09-949-016-1881	Sequence 1881, Ap
17	101	94.4	3944	4	US-09-949-016-1882	Sequence 1882, Ap
18	101	94.4	3944	4	US-09-949-016-1883	Sequence 1883, Ap
19	101	94.4	59853	4	US-09-949-016-13618	Sequence 13618, A
20	101	94.4	59853	4	US-09-949-016-13619	Sequence 13619, A
21	101	94.4	59853	4	US-09-949-016-13620	Sequence 13620, A
22	101	94.4	59853	4	US-09-949-016-13621	Sequence 13621, A
23	101	94.4	59853	4	US-09-949-016-13622	Sequence 13622, A
24	101	94.4	59853	4	US-09-949-016-13623	Sequence 13623, A
25	101	94.4	59853	4	US-09-949-016-13624	Sequence 13624, A
26	101	94.4	59853	4	US-09-949-016-13625	Sequence 13625, A
27	83	77.6	1954	1	US-08-471-570-5	Sequence 5, Appli
28	83	77.6	2676	1	US-08-471-570-7	Sequence 7, Appli
29	83	77.6	3416	2	US-08-451-822A-15	Sequence 15, Appli
30	83	77.6	3416	3	US-08-323-430-15	Sequence 15, Appli
31	81	75.7	2675	1	US-08-070-165F-5	Sequence 5, Appli
32	81	75.7	2675	2	US-08-885-418-5	Sequence 5, Appli
33	81	75.7	2681	1	US-08-070-165F-9	Sequence 9, Appli
34	81	75.7	2681	2	US-08-885-418-9	Sequence 9, Appli
35	77	72.0	2079	4	US-09-949-016-3171	Sequence 3171, Ap
36	77	72.0	2079	4	US-09-949-016-3172	Sequence 3172, Ap
37	77	72.0	2079	4	US-09-949-016-3173	Sequence 3173, Ap
38	77	72.0	2079	4	US-09-949-016-3174	Sequence 3174, Ap
39	77	72.0	2079	4	US-09-949-016-3175	Sequence 3175, Ap
40	77	72.0	2079	4	US-09-949-016-3176	Sequence 3176, Ap
41	77	72.0	2079	4	US-09-949-016-3177	Sequence 3177, Ap
42	77	72.0	2079	4	US-09-949-016-3178	Sequence 3178, Ap
43	77	72.0	2079	4	US-09-949-016-3179	Sequence 3179, Ap
44	77	72.0	2079	4	US-09-949-016-3180	Sequence 3180, Ap
45	77	72.0	110266	4	US-09-949-016-14913	Sequence 14913, A

#### ALIGNMENTS

#### RESULT 1

US-09-023-655-1288  
; Sequence 1288, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g31386
US-09-023-655-1288

Alignment Scores:
Pred. No.: 4,29e-10 Length: 2360
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-757-415A-3 (1-22) x US-09-023-655-1288 (1-2360)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1114 CACAGCCAGATGGCTGTGCACAGCTGGCCACAGAGCATCCCTCTGCGCAGACAGGTAACA 1173

Qy 21 ValSer 22
Db 1174 GTGTCT 1179

RESULT 2
US-07-997-133-2
; Sequence 2, Application US/07997133
; Patent No. 5288855
; GENERAL INFORMATION:
; APPLICANT: Bergonzoni, Laura
; APPLICANT: Mazue, Guy
; APPLICANT: Isacchi, Antonella
; APPLICANT: Roncucci, Romeo
; APPLICANT: Sarmientos, Paolo
; TITLE OF INVENTION: Extracellular Form of the Human
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/997,133
; FILING DATE: 28-DEC-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,755
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5288855man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-226-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2466
; OTHER INFORMATION:
US-08-459-296-1
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; LENGTH: 2469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-997-133-2

Alignment Scores:
Pred. No.: 4,56e-10 Length: 2469
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-07-997-133-2 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1225 CACAGCCAGATGGCTGTGCACAGCTGGCCACAGAGCATCCCTCTGCGCAGACAGGTAACA 1284

Qy 21 ValSer 22
Db 1285 GTGTCT 1290

RESULT 3
US-08-459-296-1
; Sequence 1, Application US/08459296
; Patent No. 5670323
; GENERAL INFORMATION:
; APPLICANT: No. 5670323a, Michael
; APPLICANT: Gonzalez, Ana-Maria
; APPLICANT: Baird, Andrew
; TITLE OF INVENTION: PROCESS FOR DETECTION OF NEOPLASTIC
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,296
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7573-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2466
; OTHER INFORMATION:
US-08-459-296-1
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## Alignment Scores:

Pred. No.: 4.56e-10 Length: 2469  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-459-296-1 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20  
|||||  
Db 1225 CACAGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGGCGACAGAGGTAAACA 1284  
  
Qy 21 ValSer 22  
|||||  
Db 1285 GTGTCT 1290

## RESULT 4

US-07-997-133-2  
; Sequence 2, Application US/07997133  
; GENERAL INFORMATION:  
; APPLICANT: Bergonzoni, Laura  
; APPLICANT: Mazue, Guy  
; APPLICANT: Isacchi, Antonella  
; APPLICANT: Roncucci, Romeo  
; APPLICANT: Sarmientos, Paolo  
; TITLE OF INVENTION: Extracellular Form of the Human  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
; CITY: Arlington  
; STATE: Virginia  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/997,133  
; FILING DATE: 28-DEC-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/642,755  
; FILING DATE: 18-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, Norman F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 769-226-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)521-4500  
; TELEFAX: (703)486-2347  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2469 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-997-133-2

## Alignment Scores:

Pred. No.: 4.56e-10 Length: 2469  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-757-415A-3 (1-22) x US-07-997-133-2 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20  
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Db 1225 CACAGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGGCGACAGAGGTAAACA 1284  
  
Qy 21 ValSer 22  
|||||  
Db 1285 GTGTCT 1290

## RESULT 5

US-08-451-822A-14  
; Sequence 14, Application US/08451822A  
; Patent No. 5863888  
; GENERAL INFORMATION:  
; APPLICANT: Dionne, Craig A  
; APPLICANT: Crumley, Greg  
; APPLICANT: Jays, Michael C  
; APPLICANT: Schlessinger, Joseph  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department  
; STREET: 500 Arcola Road  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/451,822A  
; FILING DATE: 26-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,430  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,372  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/549,587  
; FILING DATE: 06-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A0496B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2662 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-451-822A-14

## Alignment Scores:

Pred. No.: 5.04e-10 Length: 2662  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-451-822A-14 (1-2662)

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Db 1312 CACGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1371

Qy 21 ValSer 22  
|||||  
Db 1372 GTGTCT 1377

RESULT 6  
US-08-323-430-14  
; Sequence 14, Application US/08323430  
; Patent No. 6344546  
; GENERAL INFORMATION:  
; APPLICANT: Dionne, Craig A  
; APPLICANT: Crumley, Greg  
; APPLICANT: Jaye, Michael C  
; APPLICANT: Schlensing, Joseph  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department  
; STREET: 500 Arcola Road  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/323,430  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US to be assigned  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/549,587  
; FILING DATE: 06-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A0496  
; TELEPHONE: (215) 454-3817  
; TELEPHONE: (215) 454-3808  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2662 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-323-430-14

Alignment Scores:  
Pred. No.: 5.04e-10 Length: 2662  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-323-430-14 (1-2662)

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Db 1312 CACGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1371

Qy 21 ValSer 22  
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Db 1372 GTGTCT 1377

RESULT 7  
US-08-371-001-14  
; Sequence 14, Application US/08371001  
; Patent No. 5783683  
; GENERAL INFORMATION:  
; APPLICANT: Morrison Ph.D., Richard  
; TITLE OF INVENTION: Methods and Composition for Treating  
; Tumor Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gray Cary Ware & Freidenrich  
; STREET: 401 "B" Street, Suite 1700  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,001  
; FILING DATE: January 10, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brotman, Harris F.  
; REGISTRATION NUMBER: 35,461  
; REFERENCE/DOCKET NUMBER: P00095US0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 699-3630  
; TELEFAX: (619) 236-1048  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2733 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 210..467  
; OTHER INFORMATION: FGFR1 Alpha Exon  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 57  
; OTHER INFORMATION: "IDENTITY OF  
; OTHER INFORMATION: NUCLEOTIDE PROVISIONAL"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 117  
; OTHER INFORMATION: "IDENTITY OF  
; OTHER INFORMATION: NUCLEOTIDE PROVISIONAL"  
US-08-371-001-14

Alignment Scores:  
Pred. No.: 5.22e-10 Length: 2733  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-08-371-001-14 (1-2733)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20  
|||||  
Db 1342 CACGCCAGATGGCTGTGCACAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1401  
Qy 21 ValSer 22  
|||||  
Db 1402 GTGTCT 1407

RESULT 8  
PCT-US96-00331-14  
; Sequence 14, Application PC/TUS9600331  
; GENERAL INFORMATION:  
; APPLICANT: GENTA INCORPORATED  
; TITLE OF INVENTION: METHODS AND COMPOSITION FOR  
; TREATING TUMOR CELLS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00331  
; FILING DATE: 10 JANUARY 1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/371,001  
; FILING DATE: 10 JANUARY 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 218/068-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2733 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 210..467  
; OTHER INFORMATION: FGFR1 Alpha Exon  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 57  
; OTHER INFORMATION: "IDENTITY OF NUCLEOTIDE PROVISIONAL"  
; NAME/KEY: misc\_feature  
; LOCATION: 117  
; OTHER INFORMATION: "IDENTITY OF NUCLEOTIDE PROVISIONAL"  
PCT-US96-00331-14

Alignment Scores:  
Pred. No.: 5, 22e-10 Length: 2733  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-757-415A-3 (1-22) x PCT-US96-00331-14 (1-2733)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20  
Db 1342 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAAACA 1401

Qy 21 ValSer 22  
Db 1402 GTGTCT 1407  
RESULT 9  
US-07-631-717A-1  
; Sequence 1, Application US/07631717A  
; Patent No. 5270197  
; GENERAL INFORMATION:  
; APPLICANT: Yavon, Avner  
; APPLICANT: Ornitz, David M.  
; APPLICANT: Klagsbrun, Michael  
; APPLICANT: Leder, Philip  
; TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING  
; TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH  
; TITLE OF INVENTION: FACTOR RECEPTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/631,717A  
; FILING DATE: 19901220  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00383/018001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3503  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-631-717A-1

Alignment Scores:  
Pred. No.: 7, 27e-10 Length: 3503  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-09-757-415A-3 (1-22) x US-07-631-717A-1 (1-3503)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20  
Db 1500 CATAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAAACA 1559

Qy 21 ValSer 22

Db 1560 GTGTCA 1565

RESULT 10

US-08-166-717D-1

; Sequence 1, Application US/08166717D





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Db      2013 GAAAGT 2018
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RESULT 13
US-09-949-016-1878
; Sequence 1878, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1878
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1878

Alignment Scores:
Pred. No.:      1.17e-08      Length:      3944
Score:          101.00      Matches:      21
Percent Similarity: 95.45%      Conservative: 0
Best Local Similarity: 95.45%      Mismatches:  1
Query Match:    94.39%      Indels:      0
DB:             4          Gaps:      0

US-09-757-415A-3 (1-22) x US-09-949-016-1878 (1-3944)

Qy      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
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Db      1953 CACAGCCAGATGGCTGTGCACAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 2012

Qy      21 ValSer 22
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Db      2013 GAAAGT 2018

RESULT 14
US-09-949-016-1879
; Sequence 1879, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1879
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1879

Alignment Scores:
Pred. No.:      1.17e-08      Length:      3944
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Score:          101.00      Matches:      21
Percent Similarity: 95.45%      Conservative: 0
Best Local Similarity: 95.45%      Mismatches:  1
Query Match:    94.39%      Indels:      0
DB:             4          Gaps:      0

US-09-757-415A-3 (1-22) x US-09-949-016-1879 (1-3944)

Qy      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
|||||
Db      1953 CACAGCCAGATGGCTGTGCACAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 2012

Qy      21 ValSer 22
|||||
Db      2013 GAAAGT 2018

RESULT 15
US-09-949-016-1880
; Sequence 1880, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1880
; LENGTH: 3944
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1880

Alignment Scores:
Pred. No.:      1.17e-08      Length:      3944
Score:          101.00      Matches:      21
Percent Similarity: 95.45%      Conservative: 0
Best Local Similarity: 95.45%      Mismatches:  1
Query Match:    94.39%      Indels:      0
DB:             4          Gaps:      0

US-09-757-415A-3 (1-22) x US-09-949-016-1880 (1-3944)

Qy      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
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Db      1953 CACAGCCAGATGGCTGTGCACAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 2012

Qy      21 ValSer 22
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Db      2013 GAAAGT 2018

Search completed: February 14, 2005, 03:23:25
Job time : 40.9211 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: February 14, 2005, 03:17:13 : Search time 121.145 Seconds  
(without alignments)  
1071.529 Million cell updates/sec

Title: US-09-757-415A-3  
Perfect score: 107  
Sequence: 1 HSQAVHKLASIPLRQVTVS 22

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -OFMT=fastp -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-THRS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0  
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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
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- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
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- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	107	100.0	2360	17	US-10-641-643-1288	
2	107	100.0	2469	18	US-10-664-705-12	
3	107	100.0	2469	18	US-10-384-339C-71	
4	107	100.0	2470	17	US-10-307-817-5	
5	107	100.0	2662	16	US-10-204-041-1	
6	107	100.0	2731	17	US-10-307-817-7	
7	107	100.0	2737	17	US-10-307-817-3	
8	107	100.0	3328	15	US-10-101-510-299	
9	107	100.0	3328	18	US-10-283-975A-98	
10	107	100.0	3343	17	US-10-302-812-41	
11	107	100.0	3454	13	US-10-044-090-48	
12	107	100.0	3726	9	US-09-925-302-271	
13	107	100.0	3726	10	US-09-925-302-271	
14	107	100.0	3981	18	US-10-723-860-474	
15	107	100.0	4066	15	US-10-007-926A-182	
16	107	100.0	4066	17	US-10-159-563-305	
17	107	100.0	4444	18	US-10-723-860-5144	
18	107	100.0	4628	9	US-09-805-020-11	
19	107	100.0	5438	18	US-10-723-860-5897	
20	101	94.4	1726	13	US-10-087-192-380	
21	101	94.4	3944	13	US-10-087-192-383	
22	101	94.4	11294	10	US-09-764-891-7594	
C 22	101	94.4	15123	10	US-09-764-891-7595	
C 23	101	94.4	58215	13	US-10-087-192-379	
24	101	94.4	75853	13	US-10-087-192-382	
25	101	94.4	81.3	505	10	US-09-918-995-4697
26	87	81.3	505	10	US-09-917-800A-1466	
27	84	78.5	1451	9	US-10-384-339C-85	
28	83	77.6	2466	18	US-09-954-556-28	
29	83	77.6	2650	10	US-09-954-556-21	
30	83	77.6	2826	10	US-09-954-556-19	
31	83	77.6	2868	10	US-09-954-556-20	
32	83	77.6	2923	10	US-09-954-556-18	
33	83	77.6	2941	10	US-09-954-556-25	
34	83	77.6	3080	10	US-09-954-556-3	
35	83	77.6	3248	17	US-10-302-812-43	
36	83	77.6	3306	10	US-09-954-556-10	
37	83	77.6	4268	9	US-09-954-456-293	
38	83	77.6	4268	9	US-09-954-456-1599	
39	83	77.6	4268	10	US-09-954-556-3	
40	83	77.6	4268	11	US-09-968-007A-461	
41	83	77.6	4574	18	US-10-648-593-132	
42	80	74.8	99	16	US-10-199-820-78	
43	77	72.0	1978	13	US-10-087-192-1130	
44	77	72.0	2079	13	US-10-087-192-1133	
45	77	72.0	57561	13	US-10-087-192-1129	

ALIGNMENTS

RESULT 1  
US-10-641-643-1288  
; Sequence 1288, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/641,643  
FILING DATE: 14-Aug-2003  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1288:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 931386  
SEQUENCE DESCRIPTION: SEQ ID NO: 1288 :

US-10-641-643-1288

Alignment Scores:  
Pred. No.: 2,23e-09 Length: 2360  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-641-643-1288 (1-2360)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20  
Db 1114 CACAGCCAGATGGCTGTGCACAAAGCTGGCCAAAGCATCCCTCTCGCAGACAGGTAACA 1173  
Qy 21 ValSer 22  
Db 1174 GTGTCT 1179

RESULT 2  
US-10-664-705-12  
Sequence 12, Application US/10664705  
Publication No. US20040152107A1  
GENERAL INFORMATION:  
APPLICANT: Altar, Anthony C.  
APPLICANT: Laeng, Pascal  
APPLICANT: Young, Theresa A.  
APPLICANT: Charles, Vinod  
APPLICANT: Bukhman, Yury  
APPLICANT: Jurata, Linda  
TITLE OF INVENTION: GENE SIGNATURE OF ELECTROSHOCK THERAPY AND METHODS OF USE  
FILE REFERENCE: 03235/100M087-US2  
CURRENT APPLICATION NUMBER: US/10/664,705  
CURRENT FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: US 60/411,718  
PRIOR FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: US 60/431,882  
PRIOR FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: US 60/479,970  
PRIOR FILING DATE: 2003-06-18  
NUMBER OF SEQ ID NOS: 152  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 2469  
TYPE: DNA

ORGANISM: Rattus norvegicus  
US-10-664-705-12

Alignment Scores:  
Pred. No.: 2,37e-09 Length: 2469  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 18 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-664-705-12 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20  
Db 1225 CATAGCCAGATGGCTGTGCATTAAGCATCCCTCTCCGACAGACAGGTAACA 1284  
Qy 21 ValSer 22  
Db 1285 GTGTCA 1290

RESULT 3

US-10-384-339C-71  
Sequence 71, Application US/10384339C  
Publication No. US20040175703A1

GENERAL INFORMATION:

APPLICANT: Kreutzer, Roland  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GENE  
FILE REFERENCE: 20200/2002  
CURRENT APPLICATION NUMBER: US/10/384,339C  
CURRENT FILING DATE: 2003-03-07  
PRIOR APPLICATION NUMBER: PCT/EP02/00152  
PRIOR FILING DATE: 2002-01-09  
PRIOR APPLICATION NUMBER: DE 10100586.5  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: DE 10155280.7  
PRIOR FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: DE 10158411.3  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: DE 10160151.4  
PRIOR FILING DATE: 2001-12-07  
NUMBER OF SEQ ID NOS: 173  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 71  
LENGTH: 2469  
TYPE: DNA  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
TITLE: FGFR1  
PATENT DOCUMENT NUMBER: NM000604  
US-10-384-339C-71

Alignment Scores:  
Pred. No.: 2,37e-09 Length: 2469  
Score: 107.00 Matches: 22  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 18 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-384-339C-71 (1-2469)

Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20  
Db 1225 CACAGCCAGATGGCTGTGCACAAAGCTGGCCAAAGCATCCCTCTCCGACAGACAGGTAACA 1284  
Qy 21 ValSer 22  
Db 1285 GTGTCT 1290

RESULT 4

US-10-307-817-5  
Sequence 5, Application US/10307817

```

; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 5
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(2320)
US-10-307-817-5

Alignment Scores:
Pred. No.: 2,37e-09 Length: 2470
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-307-817-5 (1-2470)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1079 CACGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 1138
QY 21 ValSer 22
Db 1139 GTGTCT 1144

RESULT 5
US-10-204-041-1
; Sequence 1, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
; APPLICANT: STEIN-GERLACH, MATTHIAS
; APPLICANT: SALASSIDIS, KONSTANTINOS
; APPLICANT: BACHER, GERALD
; APPLICANT: MULLER, STEFAN
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion
; FILE REFERENCE: AXM-007.1P US
; CURRENT APPLICATION NUMBER: US/10/204,041
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: EP 0111858.5
; PRIOR FILING DATE: 2001-05-16
; PRIOR FILING DATE: 2001-05-16
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-041-1

Alignment Scores:
Pred. No.: 2,6e-09 Length: 2662
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-204-041-1 (1-2662)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20

; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 7
; LENGTH: 2731
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(2581)
US-10-307-817-7

Alignment Scores:
Pred. No.: 2,69e-09 Length: 2731
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-307-817-7 (1-2731)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20
Db 1340 CACGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 1399
QY 21 ValSer 22
Db 1400 GTGTCT 1405

RESULT 7
US-10-307-817-3
; Sequence 3, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 3
; LENGTH: 2737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(2587)
US-10-307-817-3

Alignment Scores:
Pred. No.: 2,69e-09 Length: 2737
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB: 17 Gaps: 0
US-09-757-415A-3 (1-22) x US-10-307-817-3 (1-2737)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1346 CACAGCCAGATGGCTGTGCACAGCTGGCCAGAGCATCCCTCTGCGCAGACAGGTAACA 1405
Qy 21 ValSer 22
Db 1406 GTGTCT 1411

RESULT 8
US-10-101-510-299
; Sequence 299, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101.510
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 299
; LENGTH: 3328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-299

Alignment Scores:
Pred. No.: 3.44e-09 Length: 3328
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-101-510-299 (1-3328)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1180 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1239
Qy 21 ValSer 22
Db 1240 GTGTCT 1245

RESULT 9
US-10-283-975A-98
; Sequence 98, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 3328

US-09-757-415A-3 (1-22) x US-10-283-975A-98 (1-3328)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1228 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1287
Qy 21 ValSer 22
Db 1288 GTGTCT 1293

RESULT 11
US-10-044-090-48
; Sequence 48, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 3454

US-09-757-415A-3 (1-22) x US-10-302-812-41 (1-3343)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1228 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1287
Qy 21 ValSer 22
Db 1288 GTGTCT 1293

Alignment Scores:
Pred. No.: 3.46e-09 Length: 3343
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-302-812-41 (1-3343)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1228 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1287
Qy 21 ValSer 22
Db 1288 GTGTCT 1293

Alignment Scores:
Pred. No.: 3.46e-09 Length: 3343
Score: 107.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-283-975A-98 (1-3328)
Qy 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1180 CACAGCCAGATGGCTGTGCACAAAGCTGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1239
Qy 21 ValSer 22
Db 1240 GTGTCT 1245

RESULT 10
US-10-302-812-41
; Sequence 41, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
; TITLE OF INVENTION: TISSUE REGENERATION
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-302-812-41
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Mon Feb 14 12:31:16 2005

QY 21 ValSer 22  
| | | | |  
Db 2011 GTGTCT 2016

Search completed: February 14, 2005, 05:18:15  
Job time : 138.145 secs

; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 474  
; LENGTH: 3981  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-474

Alignment Scores: 4.31e-09 Length: 3981  
Pred. No.: 107.00 Matches: 22  
Score: 107.00  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 18 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-723-860-474 (1-3981)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20  
| | | | |  
Db 1951 CACAGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 2010

QY 21 ValSer 22  
| | | | |  
Db 2011 GTGTCT 2016

## RESULT 15

US-10-007-926A-182  
; Sequence 182, Application US/10007926A  
; Publication No. US20030143539A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTUCCI, FRANCOIS  
; APPLICANT: HOULGATTE, REMI  
; APPLICANT: BIRNBAUM, DANIEL  
; APPLICANT: NGUYEN, CATHERINE  
; APPLICANT: VIENS, PATRICE  
; APPLICANT: FERT, VINCENT  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS  
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES  
; FILE REFERENCE: 1546-R-00  
; CURRENT APPLICATION NUMBER: US/10/007,926A  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/254,090  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 182  
; LENGTH: 4066  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: fibroblast growth factor receptor 1  
; OTHER INFORMATION: (fms-related tyrosine kinase 2, pfeiffer syndrome)  
; OTHER INFORMATION: (FGFR1) gene.  
US-10-007-926A-182

Alignment Scores: 4.43e-09 Length: 4066  
Pred. No.: 107.00 Matches: 22  
Score: 107.00  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-757-415A-3 (1-22) x US-10-007-926A-182 (1-4066)

QY 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGlnValThr 20  
| | | | |  
Db 1951 CACAGCCAGATGGCTGTGCACAAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 2010